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Yu, Misook

From:

Mosher, Marv

Sent:

Tuesday, August 19, 2003 7:22 AM

To: Subject: Yu, Misook RE: 09765086

Your judgement is better than mine in deciding whether or not there really is motivation to put the peices together, since you have read the references and I have not. If you, in your scientist role, sat down with the references, would it have occurred to you to put them together to get the invention, if you did not already know about the invention? If the invention is not a method of cancer treatment, is there an enablement issue on how to use the claimed invention for purposes other than treating cancer?

Sorry for the socratic response, but I really can't substitute my ignorance for your judgement. MM

----Original Message----From:

Yu, Misook

Sent: To:

Monday, August 18, 2003 12:38 PM

Mosher, Mary

Subject:

09765086

There are 3 sets of method claims using a chimeric construct consisting of two parts (one. prostate-targeting peptide and the other, lyis-causing anti-microbial peptide).

The first set of claim says "a method of directing an antimicrobial peptide in vivo to prostate tissue";

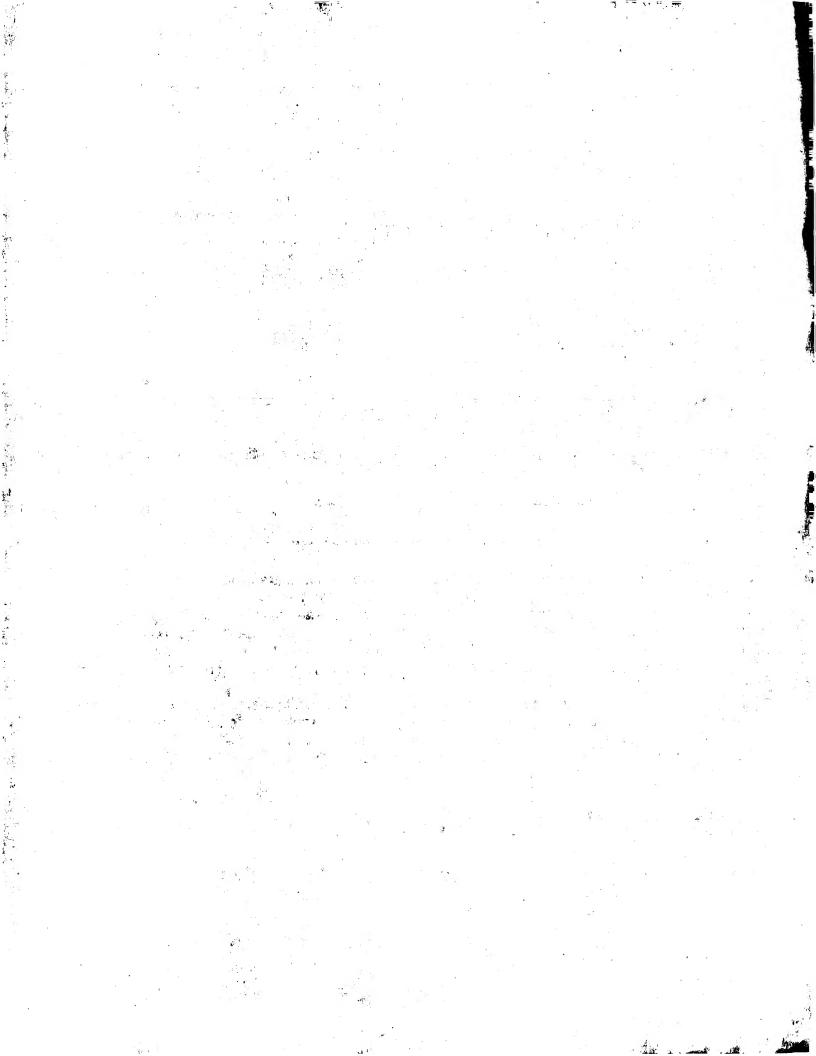
The second set of claims says "a method of inducing apoptosis in prostate tissue in vivo"; and

The third set of claims says "a method of selectively inducing apoptosis in normal prostate tissue"

The first and second sets were rejected by combination of primary reference showing prostatetargeting peptides are known in the art to direct cancer treating agents to prostate, by two types of secondary reference showing that there is a need in the prostate cancer treatment art for a method to reduce generalized side effects, and antimicrobial peptide has been used for cancer treatment. Combination of the primary and secondary references teach all necessary components of the products for directing something to prostate or inducing apoptosis in prostate.

In reply to OA, applicant argues that their invention is not drawn to method of cancer treatment and there is no motivation why one in ordinary skill would be motivated to do the purpose specified in the preamble of the claims. The most of the specification is about prostate cancer treatment using the chimeric product. Do I drop the rejection?

Examiner Misook Yu. Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)



Claim

Page 151; 193pp;

English

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AAB21907
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                                                                          The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
                                                                                                                                                                                                                                Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
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                                                                                                                                                                                                        Claim 25; Page
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                                                 prostate cancer or melanoma. The present sequence is a homing peptide isolated in the present invention, which can be conjugated to an
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                                                                                                                            The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is mouse prostate homing peptide. This sequence is useful in the homing of pro-apoptotic
                                                                                                                                                                                                                                                    Claim
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ALIGNMENTS

RESULT AAY48905

AAY48905 standard; Peptide; 7

Membrane dipeptidase-binding prostate homing peptide #21

AAY48905; 10-DEC-1999

(first entry)

Best Local Similarity 100.0%; Pred. No. 0.0029;

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Patent No. 578954
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                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                         LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0:
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 334
REFERENCE/DOCKET NUMBER:
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                                                         Application US/08944133
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504 346-8049
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Pred. No. 0.0042;
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Best Local Similarity
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INFORMATION FOR SEQ
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ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
         ZIP: 70821-2471
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
FILING DATE: 03-FEB-199
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APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
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CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                          STATE:
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REGISTRATION NUMBER: 334
REFERENCE/DOCKET NUMBER:
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P. O. Box 2471
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linear
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Pred. No. 0.0042;
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                Version #1.25
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

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Title:
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Maximum DB
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15.190 Million cell updates/sec
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US-08-944-133-25
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US-08-944-133-25
US-08-944-133-25
US-08-723-306-28
US-07-908-45A-62
US-08-434-120-08
US-08-434-120-08
US-08-431-730A-40
US-08-457-171-40
US-08-457-171-40
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US-08-689-489C-486-45
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US-09-331-730A-40
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US-09-331-730A-40
US-08-689-489C-486-45
US-09-331-840-45
US-09-331-840-845
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Sequence 27,
Sequence 25;
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Query Match
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ERENCE/DOCKET NUMBER: ONMUNICATION INFORMATIE EPHONE: 504 387-3221 EPHAX: 504 346-8049 ETAX: 504 346-8049 ETAX FOR SEQ ID NO: 6 NCE CHARACTERISTICS: STH: 14 amino acids E: amino acid E: amino acid ANDEDNESS: single OLOGY: linear ULE TYPE: peptide 133-6	BUCK BE BE	STATE: LA COUNTRY: USA ZIP: 70821-2471 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,133 FILING DATE: 06-OCT-1997 CLASSIFICATION: 5530	28 52 83.9 31 5 PCT-US94-12550-48 29 52 83.9 31 5 PCT-US95-10041-26 30 52 83.9 38 5 PCT-US95-10041-23 31 52 83.9 38 5 PCT-US95-10041-23 32 50 80.6 21 1 US-07-908-455A-64 33 50 80.6 21 1 US-07-908-455A-64 34 50 80.6 21 1 US-08-434-120-30 35 50 80.6 21 1 US-08-434-120-30 36 50 80.6 21 1 US-08-445-325-88 37 50 80.6 21 1 US-08-445-325-88 38 50 80.6 21 1 US-08-445-325-88 39 50 80.6 23 1 US-08-231-730A-24 40 50 80.6 23 1 US-08-457-7171-24 41 50 80.6 23 1 US-08-457-171-24 42 50 80.6 23 1 US-08-457-171-24 43 50 80.6 23 3 US-08-805-486-24 44 50 80.6 23 3 US-08-801-028-24 45 50 80.6 23 3 US-08-801-028-24 46 50 80.6 23 3 US-08-801-028-24 47 50 80.6 23 5 PCT-US94-06176-24
			Sequence 48 Appl Sequence 23, Appl Sequence 23, Appl Sequence 64, Appl Sequence 64, Appl Sequence 60, Appl Sequence 90, Appl Sequence 80, Appl Sequence 24, Appl

DВ 1;

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Result
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Maximum
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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PODJ_CAUCR
VM25_BORHE
Y445_CHVJI
FILS_BOVIN
TOP1_DAUGN
RBD2_HUMAN
RK2_MAIZE
VHED_BPT6
NPII_ASPOR
DNAK_METSS
TIRK_ECOLI
PPOC_TOBACC
Y458_MCTUM
Y414_ARCTUM
YA14_ARCTUM
YA14_BRCTUM
SAHH_DESCR
SAHH_PETCR
SAHH_TOBAC
SHTB_DROME
EFIA_YARLI
SAHH_TOBAC
SHTB_DROME
EFIA_YARLI
SAHH_TOBAC
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SYV_NETMM
PSCS_ORYSA
RL19_VIBCH
RL17_STRCO
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VHED_BPT4
YHA11_CRYPA
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Compugen
Q06002 bos taurus
p33119 daucus caro
p29375 homo sapien
p17788 zea mays (m
p09035 bacteriopha
p46076 aspergillus
Q32fc6 methylovoru
p08956 escherichia
c24163 nicotiana t
Q057900 methanococc
Q28069 archaeoglob
p38367 neisseria m
p43674 escherichia
p211875 borrelia he
Q27580 drosophila
p21875 borrelia he
Q27580 drosophila
p21875 brerionia li
p3253 mesembryant
Q07580 drosophila
c59949 yarrowia li
p3253 mesembryant
Q1781 petroselinu
p50248 nicotiana t
p28286 drosophila
c09klh7 neisseria m
p04426 o delta la
p09kuf7 vibrio chol
086775 streptomyce
001352 drosophila
p03695 bacteriopha
p10941 cryphonectr
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bos taurus
daucus caro
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POLY-ARG.

RP -> SA (IN REF. 2).

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; 3F064FB96B4E413D CRC64;

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SEQUENCE

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09; 77; ;	S-PROT entr the Swiss I the Swiss I ean Bioinfo non-profit and this st requires a n email to	SEQUENCE FROM N.A. STRAIN-ATCC 19089 / CB MEDLINE-21173698; Pubm Mierman W.C., Feldblyum Eisen J., Heidelberg J Potocka I., Nelson W.C DeBoy R.T., Dodson R.J., Kolonay J.F., Smit J., Utterback T., Tran K., Salzberg S.L., Shapiro "Complete genome seque Proc. Natl. Acad. Scii- CAUTION: REF. 2 SEQ FRAMESHIFTS:	CRECTED (RECTIFIED)45.	(Re	& & & & & & & & & & & & & & & & & & &
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TEL	yright. It is produc of Bioinformatics Institute. There ar Institutes as it tions as long as it is not removed. Usa agreement (See http: isb-sib.ch).	159647; Laub M.T., Paulsen Liley M.K.R., Ohta N., ron A., Stephens C., Rin A.S., Gwinn M.L., Shen M.B., Khouri H., Shen M.B., Khouri H., Shen A., Vamathevan J., Erfenter J.C., Fraser C. Caulobacter crescent. 28:4136-4141(2001). DIFFERS FROM THAT SHO	DEVELOPMENT PROTEIN. Scentus. scentus. obacteria; alpha subdivision; Caulobacter group; 4; 4; 89 / CB15; 9; PubMed=10383964; 9; PubMed=10383964; podJ expression during the Caulobacter crescentus 81:3967-3973(1999).	ALIGNMENTS PRT; 472 AA. ed) esquence update)	PROA_LACLA Y748_METJA SAHH_LEIDO Y260_SYNY3 TRME_BCMP EF1A_CRYNE SAHH_CATRO SAHH_MEDSA YMDA_BACSU DOP2_DROME ARAB_BACSU CNG4_HUMAN
	ugh a collaboratio EMBL outstation estrictions on it nt is in no wa and for commercia sb-sib.ch/announce	Maddock J.R., Maddock J.R., Phadke N.D., Ely B., Haft D.H., molaeva M., White O., M.; wN DUE TO	cter group; r crescentus cell		Q9cf73 lactococcus Q58L58 methanococc P36889 leishmania P74409 synechocyst O51830 buchnera ap O42671 cryptococcu P35007 catharanthu P50246 medicago sa O31774 bacillus su Q24563 drosophila P94524 bacillus su Q24563 drosophila

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RESULT 3
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STRAIN-SSP. HS1 SEROTYPE
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01-OCT-1993
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                                                                                                       ALKFARGGGNAGQLAKEAAKAA
                                                                                                                         SMSTARLGGKLAKLAKKLAKLA
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                                                                                                                                              10;
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      (Rel. 36, Created)
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L PROTEIN A445L.
                                                                                                                                             Conservative
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36468
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35.0%;
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                                                                                                                                            4.
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Pred.
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PROBABLE.
VARIABLE MAJOR OUTER MEMBRANE
LIPOPROTEIN 25.
                                                                                                                                                                                            N-ACYL DIGLYCERIDE (PROBABLE); 2A3EF5248D5637FD CRC64;
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20-AUG-2001 (Rel. 40, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                   Gounari F., Merdes A., Quinlan R.,
Ouzounis C.A., Georgatos S.D.;
"Boyine filensin possesses primary
to intermediate filament proteins."
                 modified
                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between \cdot the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                           SEQUENCE FROM N.A. MEDLINE=96400190; PubMed=8806566;
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Viruses; dsDNA viruses, no RNA stage;
NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                          Hess J.F.;
                                                                                                                                                                                         TISSUE=Lens;
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                                                                                                                                                                                                                       J. Cell Biol.
                                                                                                                                                                                                                                                                                                                 MEDLINE=93260017; PubMed=8491777;
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European Bioinformatics Institute
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non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib
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462 AA; 52541 MW;
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                                                                                                                                                                                                                                                                                                                                                AND PARTIAL SEQUENCE
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Phycodnaviridae; Phycodnavirus
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27;
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330-kb genome: map
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RESULT 5
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Matches 8
            DNA, FOLLOWED BY PASSAGE AND REJOINING.

-I- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NESCETIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

-I- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

-I- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                        TOP1_DAUCA P93119;
                                                                                                                -I- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
-I- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                 expression analysis in Gene 183:183-190(1996)
                                                                                                                                                                                   Carbonera D.;
                                                                                                                                                                                                     STRAIN=CV. LUNGA DI AMSTERDAM;
MEDLINE=97149297; PubMed=8996105;
                                                                                                                                                                                                                                                      Daucus carota (Carrot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
DNA TOPOISOMERASE I (EC 5.99.1.2).
                                                                                                                                                                                         Balestrazzi A.,
                                                                                                                                                                                                                           SEQUENCE FROM
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COIL 2.
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RESULT 6
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                                                                                                                                                                                Defeo-Jones D., Huang P.S., Jones R.E.,
Hanoblk M.G., Huber H.E., Oliff A.;
"Cloning of cDNAs for cellular proteins
retinoblastoma gene product.";
Nature 352:251-254(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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SMART; SM00435; TOPEUG; 1.

SMART; SM00435; TOPEUG; 1.

PROSITE; PS00176; TOPOISOMERASE_I_EUK; 1.

ISOMETASE; TOPOISOMERASE_I_EUK; 1.

ISOMETASE; TOPOISOMERASE_I_EUK; 1.

PROSITE 749 DNA CLEAVAGE (BY SIMILARITY).

SEQUENCE 790 AA; 89770 MW; CELD7DA3FF3291F5 CRC64;
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use by non-profit institutions as long as its content
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entitles requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                        RBP2."
                                                                                                                                                                                                                                                                                                                                  MEDLINE=94020841; PubMed=8414517; Fattaey A.R., Helin K., Dembski M.S., Dyson N., Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff Jones R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBB2_HUMAN P29375;
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Pfam; PF01028; Topoisomerase_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mendel; 17369; Dauca;2787;17369.
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                                                                                                                SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: TO THE C-TERMINAL THE JUMONJI PROTEIN.
                                                                                                                                                        FUNCTION: INTERACTS WITH THE RETINOBLASTOMA PROTEIN.
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9; Conservative
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70MA BINDING 1
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NDING PROTEIN 2 (RBBP-2).
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A., Defeo-Jones
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CHLOROPLAST
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Pfam;
                                                                                                                                                            J. Mol.
[3]
                                                                                                                                                                             MEDLINE-95395841; PubMed-7666415;
Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
"Complete sequence of the maize chloroplast genome:
hotspots of divergence and fine tuning of genetic in
transcript editing.";
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P17788;
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                Hoch B., Maier R.M., Appel K., "Editing of a chloroplast mRNA Nature 353:178-180(1991).
                                                                                                                                   RNA EDITING OF INITIATOR CODON. meDLINE=91367263; Pubmed=1653905;
                                                                                                                                                                                                                                                                                                            MEDLINE-90332419;
                                                                                                                                                                                                                                                                                                                       STRAIN=CV. FR9CMSSR37;
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NCBI_TaxID=4577;
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n; PF02375; jmjN; 1.
n; PF00628; PHD; 3.
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1722 AA;
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EMBL; X86563; CAA60371.1; I
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PIR; S10500; R5ZM2.
PIR; S17874; S17874.
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                                                                                                              This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its comodified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
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01-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SINGLE-STRANDED DNA BINDING PROTEIN (HELIX-DESTABILIZING
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLLINE=89016637; PubMed=3262868;
McPheeters D.S., Stormo G.D., Gosch G., Gold I
"Nucleotide sequences of the bacteriophage T2
Nucleic Acids Res. 16:9341-9342(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, T4-like phages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P09035;
01-NOV-1988
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Mendel; 11440; ZEAma; rpl2;1.
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                                                            EMBL; X12460; CAA3100
EMBL; X12460; CAA3100
PIR; S01437; DDBP32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T2
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32 OR SSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LARAAGAVAKLIAKEGKLA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IARLGGKLAKLAKKLAKLA
                                                                                                                                                                                                                                                            FUNCTION: BINDS PREFERENTIALLY TÓ SINGLE-STRANDED THEREFORE, DESTABILIZES DOUBLE-STRANDED DNA. IT IS REPLICATION, REPAIR AND RECOMBINATION. BINDS SS-DN REPLICATION FORK ADVANCES AND STIMULATES THE REPLIP PROCESSIVITY AND ACCURACY.
SUBUNIT: HOMODIMER IN THE ABSENCE OF DNA, MONOMER
                                                                                                                                                                                                                       MISCELLANEOUS: INTERACTS WITH THE POLYMERASE AND THE UVSX AND UVSY PROTEINS (BY SIMILARITY).
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                                                                           CAA31000.1;
CAA31001.1;
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Pred. No.
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BA65197231EA3CA0 CRC64;
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                                                                                                                                                                     restrictions
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Zinc-finger; METAL

Zinc. 65 78 DNA repair;

78

ZINC

(BY (BY)

SIMILARITY). SIMILARITY).

DNA-binding; HSSP;

DNA

replication;

DNA recombination;

P03695; 1GPC

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RESULT 9
VHED_PS
ID VHED_PS
AC P0979
DT 01-MA
DT METT
PT MET
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P09797;
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                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89016637; PubMed=3262868; McPheeters D.S., Stormo G.D., Gosch G., Gold L.; McPheeters D.S., Stormo G.D., Gosch G., Gold L.; Nucleotide sequences of the bacteriophage T2 and T6 Nucleic Acids Res. 16:9341-9342(1988).
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NCBI_TaxID=10666;
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32 OR SSB.
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01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SINGLE-STRANDED DNA BINDING PROTEIN (HELIX-DESTABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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MISCELLANEOUS: INTERACTS WITH THE POLYMERASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: BINDS PREFERENTIALLY TO SINGLE-STRANDED DNA AND THEREFORE, DESTABLIZES DOUBLE-STRANDED DNA. IT IS INVOLVED REPLICATION, REPAIR AND RECOMBINATION. BINDS SS-DNA AS THE REPLICATION FORK ADVANCES AND STIMULATES THE REPLISOME PROCESSIVITY AND ACCURACY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                            MSIARLGGKLAKLAKKLAKLA
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MGTAAMGGAAATAAKKADKVA 260
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Pred. No.
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Pred.
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ZINC
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                                                                                                                                                                                                                                                                                                                  replication; DNA recombination;
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                                                                                                                                                                             09EDDBCCB82AF4F6 CRC64
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                                                                          Mismatches
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48;
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DNAK_METSS
ID DNAK_M
AC Q9ZFC6
DT 20-AUG
DT 20-AUG

DNAK_METSS

STANDARD;

PRT;

641

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Q9ZFC6; 20-AUG-2001 20-AUG-2001

(Rel. 40, Created)
(Rel. 40, Last sequence update)

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RESULT 10
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Best Local S
Matches 8
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P46076;
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ACT_SITE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONDS IN INSULIN B CHAIN.
-!- COPACTOR: BINDS ONE ZINC ION.
-!- PTM: PROBABLY POSSESSES THREE DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M35 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE DEUTEROLYSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NEUTRAL PROTEASE II PRECURSOR (EC 3.4.24.39)
                                                                                                                                                                                                                                                                       PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                              Pfam; PF04104; FCYCLOTEROLYSIN.
PRINTS; PR00768; DEUTEROLYSIN.
PROSITE; PS00142; ZINC_PROTEASS; 1.
PROSITE; PS00142; ZINC_PROTEASS; 2inc; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S53810; AAB19701.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THERMOSTABLE METALLOPROTEASE. SHOWS HIGH ACTIVITIES ON BASIC NUCLEAR SUBSTRATES SUCH AS HISTONE AND PROTAMINE.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE OF BONDS WITH HYDROPHOBIC RESIDUES IN P1'; ALSO 3-ASN-|-GLN-4 AND 8-GLN-|-SER-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tatsumi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 20386;
MEDLINE=91360097; PubMed=1886621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiales; Trichocomaceae; mitosporic Trichoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001384; InterPro; IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M35.002;
                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000130; Zn_MTpeptdse
Pfam; PF02102; Peptidase_M35; 1.
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159
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GGKAAKVTKALSQLTR
                                         GGKLAKLAKKLAKLAK 23
                                                                                Similarity 50.
8; Conservative
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352
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174
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                                                                                Score 42; DB
Pred. No. 57;
4; Mismatches
                                                                                                                                                                                                        NEUTRAL PROTEBASE II.
ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                         070C5131335B7F44 CRC64;
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                                                                                               DB
57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                  Zymogen
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                                                                                                                                                                                                                                                 II.
(BY SIMILARITY).
                                                                                  4;
                                                                                                                       Length 352;
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Best Local
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                                                                                                                                                                                                                                                                        P08956;
01-NOV-1988
01-FEB-1995
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                        ECOLI
              STRAIN-KI2 / MGI655;
STRAIN-KI2 / MGI655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, So
Blattner F.R.;
                                                                                                                                                                                                                                             01-NOV-1988 (Rel. 09, Created)
01-FEB-1995 (Rel. 31, Last seq
20-AUG-2001 (Rel. 40, Last ann
TYPE I RESTRICTION ENZYME ECOK
HSDR OR HSR OR B4350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Organization K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylovorus sp. (strain Bacteria; Proteobacteria;
                                                                                         J. Mol.
                                                                                                                                                         STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00012; HSP70;
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InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. EOM C.Y., Kim Y.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=81683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylovorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel.
CHAPERONE PROTEIN
                                                                                                                  Loenen W.A.M., Daniel A.S., Braymer H.D., "Organization and sequence of the hsd gene
                                                                                                                                            MEDLINE=88118919;    PubMed=3323532;
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                             T1RK_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                          398
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SLGIETLGGVMTKLIKK 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                      N.A.
                                                                                         198:159-170(1987).
                                                                                                                                                                                                                                                                                                                            STANDARD;
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DNAK (HEAT SHOCK PROTEIN 70) (HEAT SHOCK 70 KDA
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Last annotation updat
EYME ECOKI R PROTEIN (
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; beta subdivision; Methylophilus
                                                                                                                                                                                                                       gamma subdivision;
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                            Sofia H.J.,
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                                                                                                                                                                                                                                                            cion update)
PROTEIN (EC
                                                                                                                  genes
                                                                                                                              Murray N.E.;
                            Daniels
                                                                                                                    of Escherichia coli
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region from 92
Nucleic Acids |
[3]
SEQUENCE OF 1-:
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                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benner J.S.; "Characterization and
                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / CR63;
MEDLINE-91317743;
                                                                                                                                                                                                                                                                                                                                                                                   MODIFICATION.

SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED OF THREE POLYPEPTIDES R,M AND S.

OF THREE POLYPEPTIDES R,M AND S.

MISCELLANEOUS: TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX, MULTIFUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADEMOSYL METHIONINE AND MG(2+) AS CO-FACTORS AND, IN ADDITION TO THEIR ENDONUCLEOLYTIC AND METHYLASE ACTIVITIES, ARE POTENT DNA-DEPENDENT
                                                                                                                                                                                                                                                                                                                                            ONWARD AND
                                                                                                                                                                                                                                                                                                                                          CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM ONWARD AND IS SHORTER (1090 AA) DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1650347;
Keating C.J., Moran L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the
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NP_BIND CONFLICT Complete DNA_BIND InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1. EMBL; X06545; CAA29791.1; AJ EMBL; U14003; AAA97247.1; -EMBL; AE000505; AAC77306.1; EMBL; X54198; CAA38116.1; AJ SEQUENCE Restriction system; Hydrolase; DNA-binding; ATP-binding; EcoGene; EG10459; hsdR REBASE; 980; Q00648; NDECKR. X06545; CAA29791.1; ALT_FRAME. U14003; AAA97247.1; -. proteome. 1188 ECOKI. AA; 468 496 697 40.48; 57.98; 136100 ALT_INIT WW; Score Pred. DAVKIALTATPALHTVQIFGEPVYRYTYRTAVIDGFLIDQD PPIQIITRNAQEGVYLSKGEQVERISPQ -> ECGKNRSHR H-T-H MOTIF (BY SIMILARITY).
ATP (BY SIMILARITY). RAGGGLSLQRRAGRAHQ PPIQIITRNAQEGYYLSKGEQVERISPQ -> ECGKNRSHR HPGATYCADFRRAGLPLYLPYRGYRRFSDRPGSAYSDHHPQ CC0423F2A435E578 CRC64: 42; No. DB 1; . 1.7e+02; . 5; Length 1188;

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PPOC_TOBAC
ID PPOC_T
AC 024163
DT 15-DEC
DT 15-JUL
DE PROTOP
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                                                                                                                   RESULT
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PPOC_TOBAC STANDARD: PRT; 548 AA. 024163; 024163; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR
                                                                                                                                                                 216
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                                                                                                                                                                 ARLAALEAQLAEKNAELAK
     (EC
     1.3.3.4)
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Query Match Best Local S Matches 11

Similarity

Conservative

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Mismatches

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DAGE ED DOOR
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HMGD_DF
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Best Local
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                                                      HMGD_DROME STANDARD; PRT; 112
Q05783; Q092D3;
Q1-FEB-1995 (Rel. 31, Created)
Q1-FEB-1995 (Rel. 31, Last sequence upda
Q1-FEB-1995 (Rel. 40, Last annotation up
HIGH MOBILITY GROUP PROTEIN D (HMG-D).
HMGD OR CG17950.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no resture by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by anomalistic content institutions are not removed.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=97385200; PubMed=9238074;
Lermontova I., Kruse E., Mock H.-P., Grimm B.;
"Cloning and characterization of a plastidal a
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y13465; CAA73865.1;
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Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Asteridae; euasterids I; Solar
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform of tobacco protoporphyrinogen IX oxidase.
Proc. Natl. Acad. Sci. U.S.A. 94:8895-8900(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4097;
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                                                                                                                                                                                                                                      303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: OSCILLATING EXPRESSION DURING DIURNAL GROWTH. MAXI EXPRESSION IN THE DARK PERIOD.
SIMILARITY: BELONGS TO THE PROTOPORPHYRINOGEN OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: PENULTIMATE STEP IN CHLOROPHYLL SYNTHESIS. SUBUNIT: HOMODIMER; CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SUBCELLULAR LOCATION:
DEVELOPMENTAL STAGE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: CATALYZES THE 6-ELECTRON OXIDATION IX TO FORM PROTOPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECREASED EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN ROOTS
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                                                                                                                                                                                                                                                                ARLGGKLAKLAKKLAKLAK
                                                                                                                                                                                                                                                                                                          Similarity
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peptide; Flavoprotein; FAD; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                      548
                                                                                                                                                                                                                                                                                              Conservative
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78
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57.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED IN EXPANDING PREMATURE LEAVES. IN OLDEST LEAVES. EXPRESSED AT VERY LOW
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                                                                                                                                                                                                                                                                                                         Score 41.5; DB Pred. No. le+02;
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                              Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                        Length 548;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daviss P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowley B.C., Dunkov B.C., Narias M.C., Harris M.,
RA Glodek A., Dough F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hariis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hariis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lia Z., Liang Y., Lia Z.,
RA Mcikle B.C., Kravitz S., Kulp D., Lai Z.,
RA Mcikle B.C., Kravitz S., Kulp D., Lai Z.,
RA Yella M., Walshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Yella M., Walshina N., Worley K.C., Wulb., Yang S., Yao Q.A.,
RA Yella M., Walshina M., Zhang G., Zhao Q., Zheng L.,
RA Yella P., Mary F.W., Dhola M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X., Kalla M., Lang G., Zhao Q., Zheng L.,
RA Zheng Y., Walshina M., Zhang G., 
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STRAIN=CANTON-S;
MEDLINE=94021387;
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"A high-mobility-group protein and
melanogaster.";
"HMG-D is an architecture-specific protein to DNA containing the dinucleotide TG."; EMBO J. 14:1264-1275(1995).
                                                                                                                    MEDLINE=95237208; PubMec Churchill M.E.A., Jones
                                                                                                                                                                                                                                                                                                           associated
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SEQUENCE FROM N.A.,
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he Drosophila melanogaster
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na K., Elgin S.C
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Jones D.N.M., Glaser
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SEQUENCE FROM N.A.

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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.D., Reich C.I.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,
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STRUCTURE BY NMR OF 2-74.
MEDLINE-95006330; PubMed-7922039;
Jones D.N.M., Searles M.A., Shaw G.L., Churchill M.E.A.,
Keeler J., Travers A.A., Neuhaus D.;
The solution structure and dynamics of the DNA-binding d
HMG-D from Drosophila melanogaster.";
Structure 2:609-627(1994)
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DOUBLE STRANDED DNA. PREFERS SITES CONTAINING THE SEQUENCE 5'-TTG-
3', FACILITATES DNA BENDING. ASSOCIATED WITH EARLY EMBRYONIC
CHROMATIN IN THE ABSENCE OF HISTONE H1.
-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES OF DEVELOPMENT.
-I- SIMILARITY: CONTAINS 1 HMG BOX.
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SEQUENCE
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InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
SMART; SM00398; HMG; 1.
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**IL; M77023; AAA28609.1; -.

**IL; AE00345; AAF46759.1; -.

**X A44382; A44382;

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                                                                                                                                        InterPro; IPR001048; Aakinase. Pfam; PF00696; aakinase; 1. Hypothetical protein; Complete SEQUENCE 216 AA; 24080 MW;
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                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  jannaschii.";
Science 273:1058-1073(1996).
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MHIVKIGGSLTYDAKPLLKALK
                   MSIARLGGKLAKLAKKLAKLAK
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1: sp_archea:*
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5: sp_invertebrate
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
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SUMMARIES

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Q9AAQ1	021882	Q9KY12	Q9ZMV5	Q9HT75	Q93548	Q9JY43	084119	Q9JYK0	Q9JRZ3	Q9Z902	P70906	Q9QJE6	Q9N3T9	Q9V1R8	Q53164	Q9KID1	Q9PR04	204011	ID
Q9aaq1 caulobacter	021882 bacteriopha	Q9ky12 streptomyce		Q9ht75 pseudomonas			084119 chlamydia t		Q9jrz3 chlamydia p	Q9z902 chlamydia p	P70906 borrelia he	Q9qje6 human immun	Q9n3t9 caenorhabdi	Q9v1r8 pyrococcus	Q53164 rhodobacter	Q9kid1 borrelia he	Q9pr04 ureaplasma	Q04011 wuchereria	Description

ALIGNMENTS

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RESULT 2 Q9PR04 ID Q9PR04 PRELIMINARY; PRT; 981 AA. AC Q9PR04; PRELIMINARY; PRT; 981 AA. DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-CT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DE P115 PROTEIN.	Query Match 45.2%; Score 47; DB 5; Length 459; Best Local Similarity 45.5%; Pred. No. 87; Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0; 2 MSIARLGGKLAKLAKLAKLAK 23 1	RESULT 1 004011 D Q04011; 10 Q04011; 20 Q04011; 21 Q04011; 22 Q04011; 23 Q04011; 24 Q04011; 25 Q04011; 26 Q04011; 27 Q04011; 28 Q04011; 29 Q1 CTEMBLrel. 01, Created) 29 Q1 NOV-1998 (TTEMBLrel. 01, Last sequence update) 20 Q1 NOV-1998 (TTEMBLrel. 08, Last sequence update) 20 Q1 NOV-1998 (TTEMBLrel. 08, Last annotation update) 21 Q1 NOV-1998 (TTEMBLrel. 08, Last annotation update) 22 MYOSIN-LIKE PROTEIN (FRAGMENT). 23 WUChereria bancroftl. 20 WUChereria bancroftl. 21 Q1 Wuchereria. 22 Q1 Chromadorea; Spirurida; Filarioidea; 23 Q1 Chromadorea; Spirurida; Filarioidea; 24 Q1 Chromadorea; Spirurida; Filarioidea; 25 Q1 Chromadorea; Spirurida; Filarioidea; 26 Q1 Chromadorea; Spirurida; Filarioidea; 27 Q1 Chromadorea; Spirurida; Filarioidea; 28 Q1 Chromadorea; Spirurida; Filarioidea; 29 Q1 Chromadorea; Spirurida; Filarioidea; 20 Q1 Chromadorea; Spirurida; Filarioidea; 21 Q1 Chromadorea; Spirurida; Filarioidea; 21 Q1 Chromadorea; Spirurida; Filarioidea; 21 Q1 Chromadorea; Spirurida; Filarioidea; 22 Q1 Chromadorea; Spirurida; Filarioidea; 23 Q1 Chromadorea; Spirurida; Filarioidea; 24 Q1 Chromadorea; Spirurida; Filarioidea; 24 Q1 Chromadorea; Spirurida; Filarioidea; 25 Q1 Chromadorea; Spirurida; Filarioidea; 26 Q1 Chromadorea; Spirurida; Filarioidea; 26 Q1 Chromadorea; Spirurida; Filarioidea; 27 Q1 Chromadorea; Spirurida; Filarioidea; 28 Q1 Chromadorea; Spirurida; Filarioidea; 29 Q1 Chromadorea; Spirurida; Filarioidea; 20 Q1 Chromadorea; Spirurida; Filarioidea; 21 Q1 Chromadorea; Spirurida; Filarioidea; 21 Q1 Chromad

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SEQUENCE
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"Surface protein variation by expression site
relapsing fever agent Borrelia hermsii.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AF230049; AAF73349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02483; SMC_C; 1.
Pfam; PF02463; SMC_N; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
COMPLETE PROCEOME.
SEQUENCE 981 AA; 111673 MW; 119100B1C9880
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EMBL; AE002114; AAF30546.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
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Bacteria; Firmicutes;
Mycoplasmataceae; Ure
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Plasmid 1p28.
Bacteria; Spiroch
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MEDLINE=20500219;
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witz E.J., Glass
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Q1.MAY-1999 (Trembl.r
Q1.JUN-2001 (Trembl.r
UPTAKE HYDROGENASE.
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01-MAY-2000
01-JUN-2001
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"Isolation of regulatory mutants in photosynthesis gene expression Rhodobacter spheroides 2.4.1 and partial complementation of a Prrf mutant by the HupT histidine-kinase.";
Microbiology 141:1805-1819(1995).
EMBL; Y14197; CAA74585.1; -.
EMBL; Y14197; CAA74585.1; -.
EMBL; Y14197; CAA74585.1; -.
EMBL; Y14197; CAA74585.1; -.
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Submitted (
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                                                                                                 "pyrococcus abyssi genome sequence: insights i structure and evolution."; submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL; AJ248284; CAB49281.1; -. InterPro; IPR003405; SMC_C.
InterPro; IPR003405; SMC_N.
                                                                                                                                                                                                                      Pyrococcus abyssi.
Archaea; Euryarchaeota;
NCBI_TaxID=29292;
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Rhodobacter sp
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"The sequence of C. &
Submitted (MAR-2000)
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01-OCT-2000 (TremBLrel.
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Y47G6A.12 PROTEIN.
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"Genetic analysis of HIV-1 Spanish isolates."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF152816; AAF08454.1; -. InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                          Human immunodeficiency virus Viruses; Retroid viruses; Ret NCBI_TaxID=11676;
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STRAIN-BRISTOL N2;
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Rhabditidae; Peloderinae;
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                                                "Comparative genomes of Chlamydia Nat. Genet. 21:385-389(1999).
EMBL, AE001604; AAD18335.1; -.
HSSP, P24182; IBNC.
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01-FEB-1997
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SEQUENCE
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Bacteria; Chlamydiales;
NCBI_TaxID=83558;
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Pfam; PF00921; Lipoprotein_2; 1.
SEQUENCE 360 AA; 36906 MW; 8620
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Restrepo B.I., Carter C.J.,
Submitted (MAR-1996) to the
EMBL; U52149; AAB17739.1;
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VARIABLE MAJOR PROTEIN 1
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Bacteria; Spirochaetales;
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Pfam; PF0
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Pro; IPRO00901; CPSase.
PF00289; CPSase_L_chain; 1.
TE; PS00867; CPSASE_2; UNKNOWN_1.
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R.S.;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BIOTIN CARBOXYLASE (ACETYL-COENZYME A CARBOXYLASE,
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PROSITE; PS00867; CPSASE_2; UNKNC
SEQUENCE 454 AA; 50092 MW; 9D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequences of Chlamydla trachomatis pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AP002545; BAA98392.1;
EMBL; AE002217; AAF38404.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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     PROTEIN,
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13; Conser
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454 AA;
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[N, PUTATIVE.
                                                                                                                           PRELIMINARY;
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Pred. No.
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Last sequence update)
Last annotation updat
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RESULT Q9JY43 ID Q9

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Q9JY43

PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:1809-1815(2000).
EMBL; AE002505; AAF41903.1;
TIGR; NMB1548; -
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                      Chlamydia trachomatis. Bacteria; Chlamydiales;
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01-NOV-1998 (TrEMBLIEL 08, La
01-NOV-1998 (TrEMBLIEL 13, La
01-MAY-2000 (TrEMBLIEL 13, La
HYPOTHETICAL 10.4 KDA PROTEIN.
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01-NOV-1998
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MEDLINE=20175755;
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STRAIN=MC58 / SEROGROUP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup Bacteria; Proteobacteria; beta sub
                                                                                                       Science 282:754-759(1998).
EMBL; AE001285; AAC67708.1; -.
Hypothetical protein; Complete
SEQUENCE 104 AA; 10436 MW;
                                                                                                                                                    "Genome sequence of an obligate Chlamydia trachomatis.";
                                                                                                                                                                                      Stephens R.S., Kalman S., Mitchell W.P., Olinger L.,
                                                                                                                                                                                                                                                                                                                                                                   084119
                                                                                                                                                                            Davis R.W.;
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Last sequence update)
Last annotation update)
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Pred. No. 3.3e
4; Mismatches
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                                              core 43; DB red. No. 66; Mismatches
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Q93548;
Q1-FEB-1997
Q1-FEB-1997
Q1-FEB-1997
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STRAIN-MC58 / SEROGROUP B;

MEDILINE-20175755; PubMed-10710307;

MEDILINE-20175755; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Nelson W.C., Gwinn M.L., DeBoy R., Fleischmann R.D., Dougharty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougharty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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01-OCT-2000
01-OCT-2000
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                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                            elegans.";
Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:1809-1815(2000).
EMBL; AE002525; AAF42096.1;
TIGR; NMB1755; -.
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  Z81016; CAB02663.1;
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L PROTEIN NMB1755.
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47.68;
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subdivision; Neisseriaceae; Neisseria.
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01-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                    Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001965; Pfam; PF00628; PHD; SMART; SM00249; PHD;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE004962; AAG08883.1; -.
InterPro; IPR001987; Lipoprotein_4.
Pfam; PF01297; Lipoprotein_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE
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149 GKIAKVDKKTAKTVK 163
                                                                                                                                                                                                                                                            Local Similarity
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9; Conserv
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Last annotation updat
                                                                                                                                                                                                                            Score 43; Db 2, 2. Pred. No. 2.1e+02; 5;
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Page

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 8, 2002, 13:33:37; Search time 12.86 Seconds (without alignments) 136.238 Million cell updates/sec

Title: Perfect score:

CHIMERA 104 1 SMSIARLGGKLAKLAKKAK 23 Sequence:

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		on one			SUMMAKIES	
NO.	Score	Match	Match Length	B	DI	Description
-	47		981	7	C82930	pl15 protein UU140
7	45	43.3	362	7	140304	outer membrane lip
m	45	43.3	462	~	T17948	ABC transporter pr
4	45	43.3	1117	7	B75150	(1)
Ŋ	44	42.3	454	~	E72110	biotin carboxylase
9	44	42.3	454	~	F86513	biotin carboxylase
7	44	42.3	454	7	G81560	acetyl-coenzyme A
œ	43.5	41.8	548	7	A81070	tspB_protein, prob
6	43	41.3	104	~	H71555	
10	43	41.3	114	~	B81046	
11	43	41.3	246	~	T21215	
12	43	41.3	307	~	C82959	O)
13	43	41.3	337	ď	C70990	hypothetical prote
14	43	41.3	412	7	D71972	hypothetical prote
15	43	41.3	755	~	S32103	
16	43	41.3	190	~	JC5749	DNA topoisomerase
17	43	41.3	1722	Н	178879	retinoblastoma bin
18	42	40.4		~	A75254	conserved hypothet
19	42	40.4		Н	R5ZM2	ribosomal protein
20	42	40.4	29	Н	DDBP32	helix-destabilizin
21	42	40.4	293	Н	DDBP36	helix-destabilizin
22	42	40.4	352	~	S16547	neutral proteinase
23	42	40.4	45	N	H71553	probable biotin ca
24	42	40.4	45	~	D81708	acetyl-coenzyme A
25	43	40.4		7	S63652	hypothetical prote
56	42	40.4	953	~	S75285	methyl-accepting c
27	43	40.4	Н	-	NDECKR	type I site-specif
28	42	40.4	1616	~	T47801	hypothetical prote
59	42	40.4	m	7	T42567	tegument protein 2

protoporphyrinogen high mobility grou	hypothetical prote hypothetical prote	conserved hypothet adenosylhomocystei	outer membrane cla	hypothetical prote	outer membrane pro	outer membrane pro	probable heat shoc	cmk protein precur	hypothetical prote	hypothetical prote	DNA repair protein	variable major pro
T04058 A44382	A75187 B64357	F69526 T15035	A37004	T27867	A81782	C81205	F85616	D64830	B86133	G96590	T43507	S11981
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548 112	140 216	221	240	241	242	242	262	262	293	353	354	364
39.9 39.4	39.4 39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4
41.5	4 1	41	41	41	41	41	41	41	41	41	41	41
30 31	3.2 3.3 5.0	3 34 5 4	36	37	38	39	40	41	42	43	44	45

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RESULT

C82930
p115 protein UU140 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C; Accession: C82930
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
A; Reference number: A82870
A; Accession: C82930
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-981 <gla></gla>
A; Cross-references: GB: AE002114; GB: AF222894; NID: 96899086; PIDN: AAF30546.1; GSPDB: GN
A; Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: p115; UU140
A; Genetic code: SGC3
Query Match 45.2%; Score 47; DB 2; Length 981;
Best Local Similarity 52.4%; Pred. No. 71;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 3 SIARLGGKLAKKLAKKAK 23
Db 188 NLARLNDIVANLKKELAKLQK 208

RESULT 140304

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Score 45; DB 2; Length 362; Pred. No. 55; 4; Mismatches 8; Indels Query Match 43.3%; Best Local Similarity 45.5%; Matches 10; Conservative

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Gaps ; 0

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Octoring A carboxylase, biotin carboxylase CP0586 [imported] - Chlamydophila p C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A; Reference number: A81500; MUID:20150255
A; Accession: G81560
A; McCession: G81560
A; Residues: 1-454 <REA>
A;Reference number: A72000; MUID:99206606
A;Accession: E72110
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <ARNN
A;Residues: 1-454 <ARNN
A;Experimental source: Strain CWL029
C;Genetics:
C;Genetics:
C;Genetics: acc
C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;3-448/Domain: biotin carboxylase homology <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biotin carboxylase [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F86513
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
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A;Experimental source: strain AR39, HL cells
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A) Status: preliminary
A) Molecule type: DNA
A) Residues: 1-454 <STO>
A) Cross-references: GB: BA000008; NID: g8978555; PIDN: BAA98392.1; GSPDB: GN00142
A) Experimental source: strain J138
C) Genetics:
A) Genetics
C) Superfamily: biotin carboxylase; biotin carboxylase homology
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A;Gene: CP0586
C;Superfamily: biotin carboxylase; biotin carboxylase homology
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Pred. No. 93;
2; Mismatches
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93;
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Pred. No.
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nilarity 56.5%;
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Best Local Similarity 56.5%;
Matches 13; Conservative
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Matches 13; Conserv
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R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A; Reference number: A75001
A; Accession: B75150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1177 <KAW>
A,Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49281.1; PID:9545779
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E7210
biotin carboxylase - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: E72110
R;Kalman, S.: Mitchell, W.: Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome segregation protein (smc1) PAB2109 - Pyrococcus abyssi (strain Orsay) C; Species: Pyrococcus abyssi C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96813.1 A;Experimental source: specific host Chlorella strain NC64 C;Genetics: A;Note: A45L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB;
Pred. No. 68;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 MGVIKSGGSVARLKKAIPKIKK 330
                                                      :: || || :|||| 268 ALKFARGGGNAGQLAKEAAKAA 289
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                                1 SMSIARLGGKLAKLAKKLAKLA 22
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Best Local Similarity 30.1.
Best Local 8; Conservative
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Best Local Similarity 50.0
Matches 10; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <TET>
A;Residues: 1-114 <TET>
A;Cross-references: GB:AE002525; GB:AE002098; NID:g7227004; PIDN:AAF42096.1; PID:g722
A;Experimental source: serogroup B, strain MC58
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C;Species: Pseudomonas aeruginosa
C;Decies: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C82959
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
                                                                                 C; Accession: B81046
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755
  hypothetical protein NMB1755 [imported] - Neisseria meningitidis (strain MC58 serogro
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A;Cross-references: EMBL:281016; PIDN:CAB02663.1; GSPDB:GN00028; CESP:F21G4.4
A;Experimental source: clone F21G4
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21215
                               C.Species: Neisseria meningitidis
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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llarity 47.6%; Pred. No. 36;
Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Mortimore, B. submitted to the EMBL Data Library, October 1996 A;Reference number: 219392 A;Accession: T21215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 73;
2; Mismatches
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A; Introns: 31/3; 113/3; 175/3; 197/3
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55 AIADLAGEMRRLAKKSKMLLK 75
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                  ESPECIATION, probable NMB1548 [imported] - Neisseria meningitidis (strain MC58 serogrou C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Saccession: A81070
R; Tettelin, H: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Aluthors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Neference number: A81000; MUID:20175755
A; Accession: A81070
A; Accession: A81070
A; Accession: A81070
A; Astaus: preliminary
A; Molecule type: DNA
A; Residues: 1-548 <TETY
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A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1548
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R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A;Reference number: A71570; MUID:99000809
A;Accession: H71555
A;Accession: H71555
A;Status: preliminary
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A;Experimental source: serotype D, strain UW-3/Cx
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C; Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 28-Jul-2000
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A,Gene: CT117
C,Superfamily: Chlamydia trachomatis hypothetical protein CT117
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     Length 454;
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                                                            6; Indels
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Pred. No. 1.3e+02;
4; Mismatches 6;
Score 44; DB 2;
Pred. No. 93;
2; Mismatches
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                                                                                                                                                 106 SESIAMMGDKIA--AKSLAKKIK 126
                                                                                                              1 SMSIARLGGKLAKLAKKLAK 23
  42.3%;
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Best Local Similarity 44.4%;
Matches 12; Conservative
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                                                          13; Conservative
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Matches 10; Conserva
                               Best Local Similarity
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     Query Match
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                                                    Matches
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Gaps

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41.3%; Score 43; DB 2; Length 412; 38.1%; Pred. No. 1.2e+02;

6; Mismatches

8; Conservative

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A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0110
C;Superfamily: Helicobacter pylori hypothetical protein HP0120
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Matches 8; Conserv
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Job time: 124 sec
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A;Experimental source: strain PAO1
C;Genetics
A;Gene: PAO498
C;Superfamily: hypothetical protein H10119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-412 <ARN>
A;Cross-references: GB:AE001450; GB:AE001439; NID:g4154617; PIDN:AAD05689.1; PID:g415461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein jhp0110 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Jun-2000
C;Accession: D71972
S;Accession: D71972
S;Anlm, K.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A,Reference number: A71800; MUID:99120557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Species: Mycobacterium tuberculosis
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2
Pred. No. 90;
2; Mismatches
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A; Reference number: A82950; MUID:20437337
A; Accession: C82959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.3%;
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Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.00,
The State of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 RLGGLDGKLRERLGKLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Rv3128c
A;Start codon: GTG
F;194/Region: amber stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RLGGKLAKLAKKLAKLA 22
                                                                                                                                                           A; Residues: 1-307 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                 A;Status: preliminary
                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: D71972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics
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C70990
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Nitherant anames: intermediate filament protein
(Species: Bos primigenius taurus (cattle)
(Species: Bos primigenius taurus taurus)
(Species: Bos primigenius taurus)
(Species: Bos primigenius taurus)
(Species: Bos primigenius taurus)
(Species: Bos preliminary)
(Species: Britian taurus)
(Species: 
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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50.0%;
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Best Local Similarity 50.v.
1.20 8; Conservative
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431 GGKISKAFEKLGKMIK 446
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filensin - bovine
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8, 2002, 13:35:41

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 13:25:12 ; Search time 12.46 Seconds (without alignments) 41:539 Million cell updates/sec Run on:

CHIMERA 104 1 SMSIARLGGKLAKLAKKLAKLAK 23 Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

212252 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	Sequence 7, Appli	4,	8		26,	3, 1	Sequence 6, Appli	4	30	m	27,	Sequence 27, Appl	28,	28,	'n		28,	54,	Sequence 28, Appl	54,		69	38,		39,		Sequence 25, Appl
Sorman	ai ai	US-08-944-133-7	US-08-944-133-4	US-08-944-133-8	US-08-944-133-27	US-08-944-133-26	US-08-944-133-3	US-08-944-133-6	US-07-908-455A-4	US-08-434-120-30	US-08-465-325-30	US-08-723-306-27	PCT-US96-10041-27	US-08-723-306-28	PCT-US96-10041-28	US-07-908-455A-2	US-07-908-455A-28	US-08-434-120-28	US-08-434-120-54	US-08-465-325-28	US-08-465-325-54	US-07-908-455A-43	-120	-133	-133-2	133-3	US-08-944-133-43	US-08-944-133-25
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ap (Query Match	69.2	69.2	69.2	69.2	64.4	63.5	59.6	59.6	59.6	59.6	29.6	59.6	58.7	58.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	57.7	55.8	55.8	55.8	55.8	54.8
	Score	72	72	72	72	67	99	62	62	62	62	62	62	61	61	9	09	9	9	9	09	09	09	58	28	28	28	57
	No.	-	7	m	4	S	9	7	60	Φ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

69.2%; Score 72; DB 1; Length 21;

Query Match

Sequence 15, Sequence 41, Sequence 47, Sequence 27, Sequence 53, Sequence 53, Sequence 59, Sequence 59, Sequence 69, Sequence 40, Seque	· ·	
US-07-908-455A-15 US-08-444-120-41 US-08-465-325-41 US-07-908-455A-27 US-07-908-455A-33 US-07-908-455A-62 US-08-434-120-59 US-08-434-120-59 US-08-434-120-59 US-08-455-325-59 US-08-465-325-59 US-08-465-325-59 US-08-467-321-40 US-08-457-171-40 US-08-891-730A-40	ALIGNMENTS 3 5 Peptides 1.0, Version #1.25 4,133 7,7 1,075 2,525 2,525 4, File No. 5789542 9	
57 54.8 21 1 1 6 6 5 3 .8 2 1 1 1 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 1 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 5 3 .8 2 3 1 1 6 6 6 6 5 3 .8 2 3 3 1 6 6 6 6 5 3 .8 2 3 3 1 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	TOP	7
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Length 28;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFA: 504 346-8049
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
CLASSIFICATION NUMBER: 08/789,077
FILING APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-APR-1994
ATTONREY/AGERT INPOMMATION:
NAME: REDISTRATION NUMBER: 33451
REGISTRATION NUMBER: 33451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
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80.0%; Pred. No. 0.00033;
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Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Amphipathic Peptides NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
2IP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: John H. Runnels
STREET: P. O. BOX 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IARLGGKLAKLAKKLAKLAK 23
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                                                                                                                                            COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                      Baton Rouge
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Matches 16; Conserve
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US-08-944-133-27
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                                                                                                      CITY: B
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                          Gaps
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  Best Local Similarity 80.0%; Pred. No. 0.00025; Matches 16; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UPERALIUN SISTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/22,525
FILING DATE:
APPLICATION NUMBER: US/08/22,525
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Pred. No. 0.00033;
                                                                                                                                                                                                     Sequence 4, Application US/08944133
Sequence 4, Application US/08944133
Batent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STRRET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-944-133-8; Sequence 8, Application US/08944133; Patent No. 5789542
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APPLICANT: Becker, Calvin L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: At
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                               4 IARLGGKLAKLAKKLAKLAK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 IARLGGKLAKLAKKLAKLAK 23
                                                                                     2 LAKLAKKLAKLAKKLAKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Runnels, John H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: LA
                                                                                                                                                                    RESULT 2
US-08-944-133-4
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                                                                                                                                                                                                                                                    Score 67; DB 1; Length 21;
Pred. No. 0.0013;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 1; Length 21; Pred. No. 0.0017; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTOKNEY/AGENT INFORMATION:
NAME: RUnnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TTTLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. BOX 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-OCT-1997
CLASSIPICATION: 5330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FBB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08944133 Patent No. 5789542
                                                                                                                                                                                                                                                           64.48;
78.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 504 346-8049 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                        4 IARLGGKLAKLAKKLAKLA 22
                                                                                                                                                                                                                                                                                                                                                                                3 LAKLAKKLAKLAKKA 21
        TELERAX: 504 J. INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TRNGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.5
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-944-133-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-944-133-3
                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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JS-08-944-133-3
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                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: RUNNels, John H
REGISTRATION NUMBER: 33451
FELECOMMULICATION NUMBER: Atty File No. 5789542 9301
TELECOMMULICATION INFORMATION:
TELEPHONE: 504 387-3221
INFORMATION FOR SEQ ID No: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Score 72; DB 1; Length 28; 80.0%; Pred. No. 0.00033; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 70821-2471
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION NUMBER: 08/789,077
FILING DATE: 03-PEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/08944133
Sequence 26, Application US/08944133
Fatent No. 5789542
GENERAL INFORMATION:
TAPPLICANT: McLaughlin, Mark L.
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                   FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/944,133
                                     CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33451
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Best Local Similarity 80.03
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Runnels, John H
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-944-133-26
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Length 21;
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Sequence 30, Application US/08434120

Fatent No. 5633479

GENERAL INFORMATION:
APPLICANT: Baker, Margaret A. APPLICANT: Jacob, Leonard S. APPLICANT: Tacker S. APPLICANT: Treatment of Gynecological TITLE OF INVENTION: Malignancies with TITLE OF INVENTION: Biologically Active Peptides NUMBER OF SEQUENCES: 117

CORRESPONDENCES: 117

ADDRESSEE: Carcila, Byrne, Bain, Gilfillan, STREET: General & Stewart STREET: General Stewart

CITY: Roseland

STATE: New Jersey

COUNTRY: USA
TITLE OF INVENTION: USES Therefor NUMBER OF SEQUENCES: 89
CORRESPONDENCE: ADDRESS:
ADDRESSER: Carella, Byrne, Bain, Gilfillan, ADDRESSER: Cacchi & Stewart STARET: New Jersey
COUNTRY: USA

ZIRET: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARR: DM4.V2
OPERATING DATE: 1920702
CLASSIFICATION NUMBER: US/07/908,455A
FILING DATE: 1930702
FILING DATE: 195-APR-1991
APPLICATION NUMBER: US 07476629
FILING DATE: 08-FBB-1990
ATTORNEY/AGENT INFORMATION:
NAME: O1Stein, Elliot M
RESTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
REFECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMINO ACID
STRANDEDNESS:
TYPE: AMINO ACID
STRANDENDENSS:
TYPE: AMINO ACID
STRANDENMESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1;
Pred. No. 0.0064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: amide-terminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vuery Match 59.6%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RLGGKLAKLAKLAKLA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07068
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-434-120-30
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APPLICANT: Berkowitz, Barry A.
APPLICANT: Rari, U. Prasad
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: No. 5459237el Peptide Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.6%; Score 62; DB 1; Length 14; 100.0%; Pred. No. 0.0044; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELECHNORE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 0.271

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
APPLICATION NUMBER: US/08/681,075
                                                                                                                                                                                                                   Sequence 6, Application US/08944133
Patent No. 5/89542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
ITILE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. BOX 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-07-908-455A-4
; Sequence 4, Application US/07908455A
; Patent No. 5459237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                              Query Match 59.6
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 KLAKLAKKLAKLAK 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Patent No. 5856178
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White Phb, Wanneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                        Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1; Len
Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.6%; Score 62; DB 2;
                                                                                                    REFERENCE/DOCKET NUMBER: 05387.0021-03000 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4400 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. BOX 2550
CITY: Salt Lake City
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SWELGETT PID. SUSAN
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
      07/891,201
                                                                                   32,984
                                                                                                                                                                                                                                                                                                                                                                          59.6%;
                     FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORGLS, Jean B
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.4'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RLGGKLAKLAKKLAKLA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-30
      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-723-306-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.6%; Score 62; DB 1; Length 21; 82.4%; Pred. No. 0.0064; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 510 Campus Drive
APPLICANT: 510 Campus Drive
APPLICANT: 510 Campus Drive
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I. Street, N.W. Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TIPE: FIDEPY GISA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                             SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/08/226,108
FILING DATE:
APPLICATION NUMBER: US/07/937,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/08465325 Patent No. 5686563 GENERAL INFORMATION:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RLGGKLAKLAKKLAKLA 22
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-434-120-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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PCT-US96-10041-28
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                                                    STATE: U COUNTRY:
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                    Gaps
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APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SQUENCES:
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
CTTY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/08723306
Patent No. 5856178
GENERAL INFORMATION:
APPLICANT: White Phb, Woneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                  4; Indels
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APPLICATION NUMBER: PCT/US96/10041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 5;
Pred. No. 0.007;
Best Local Similarity 70.0%; Pred. No. 0.007;
                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.6%; Sc
Best Local Similarity 70.0%; Pr
Matches 14; Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015321922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
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                                                                                      2 LKKLAKKLKKLAKLAKLAK 21
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               14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: TELEFAX: 8
                                                                                                                                            RESULT 12
PCT-US96-10041-27
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US-08-723-306-28
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                  Matches
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Gaps
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GENERAL INFORMATION:
APPLICANT: White Phb, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Trask Britt and Rossa STREET: P.O. Box 2550 CITY: Salt Lake City STATE: Utah
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATORNEY/ACENT INFORMATION:
NAME: SWEIGET PhD, Susan E
RELISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUICATION INFORMATION:
TELEPHONE: 8015319168
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
STRANDEDNESS:
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Best Local Similarity 77.8
Matches 14; Conservative
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APPLICANT: Kari, U. Prasad
APPLICANT: Maloy, W. Lea
APPLICANT: Maloy, W. Lea
TITLE OF INVENTION: U. 0. 5455237e1 Peptide Compositions and
TITLE OF INVENTION: U. 0. 5455237e1 Peptide Compositions and
TITLE OF INVENTION: U. 0. 5455237e1 Peptide Compositions and
TITLE OF INVENTION: U. 0. 545037e1 Peptide Compositions and
TITLE OF INVENTION: U. 0. 564041
ADDRESSEE: Carcella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carcella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carcella, Byrne, Bain, Gilfillan,
STREET: Now Jersey
COUNTY: U. 0. 6 Seeker Farm Road
CITY: Roseland
STREET: Now Jersey
COUNTY: U. 0. 6 Seeker Farm Road
CITY: Now Jersey
COUNTY: U. 0. 6 Seeker Farm Road
CITY: Now Jersey
COUNTY: U. 0. 6 Seeker Farm Road
CITY: Now Jersey
COUNTY: U. 0. 6 Seeker Farm Road
COUN
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Pred. No. 0.0097;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07908455A; Patent No. 5459237; GENERAL INFORMATION:
                                                                       28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.7%;
Best Local Similarity 77.8%;
Matches 14; Conservative
                          | INFORMATION FOR ESQ ID NO: 28
| SEQUENCE CHARACTERISTICS: | EENGTH: 23 amino acids | TYPE: amino acid | STRANDEDNESS: | TOPOLOGY: not relevant | MOLECULE TYPE: peptide | HYPOTHERICAL: YES | PCT-US96-10041-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 RLGGKLAKLAKKLAKLAK 23
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8015321922
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US-07-908-455A-2
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      Query Match
      57.7%; Score 60; DB 1; Length 21;

      Best Local Similarity 57.9%; Pred. No. 0.012;

      Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

      Qy 4 IARLGGKLAKLAKKLAKLA 22

      Db 2 IAKIAGKIAKIAKIAKIA 20
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Search completed: May 8, 2002, 13:34:22 Job time: 550 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 8, 2002, 07:20:14; Search time 35.89 Seconds

(without alignments)
28:529 Million cell updates/sec

Perfect score: 30-765-086-207

Sequence: 1 SMSIARL 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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1: SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_vortebrate:*
13: sp_vortebrate:*
14: sp_unclassified:*

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P77850 chlamydia t	084705 chlamydia t	Q9plm7 chlamydia m	Q9c6f0 arabidopsis	065663 arabidopsis	Q9yct2 aeropyrum p	068069 rhodobacter	Q9cse0 mus musculu	Q90417 brachydanio	Q9bu29 homo sapien	Q12205 saccharomyc	Q9h0h0 homo sapien	Q9uld3 homo sapien	Q9syi4 arabidopsis	Q85057 peanut stri	Q85071 peanut stri	Q9u175 leishmania	097096 clonorchis	Q9zwb5 arabidopsis
SUMMARIES	ID	P77850	084705	Q9PLM7	Q9C6F0	065663	O9YCT2	690890	O3CSEO	Q90417	Q9BU29	012205	0н0н60	O9ULD3	Q9SY14	085057	085071	Q9U175	960460	09ZWB5
	DB	7	7	7	19	10	-	7	1	13	4	٣	4	4	10	12	12	S	S	10
	Query Match Length DB	301	301	301	329	369	305	307	317	422	571	849	1204	1209	1216	3222	3222	3475	212	213
dР	Query Match	90.0	90.0	90.0	90.0	90.0	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	86.7	83.3	83.3
	Score	27	27	27	27	27	26	26	26	26	26	26	26	26	26	56	26	26	25	25
	Result No.	1	7	٣	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

013888 schizosacch P92175 drosophila P91933 drosophila P91935 drosophila P91935 drosophila Q91128 pseudomonas Q55529 synechocyst Q9m2b7 arabidopsis Q9rj38 streptomyce O6427 chlorella v O9emq2 amsacta moo Q9vh3 drosophila O4843 bacteriopha Q9vh3 drosophila O4843 bacteriopha Q91195 pseudomonas Q52607 agrobacteri Q64748 avian adeno	7
255 3 013888 259 5 P92175 259 5 P91933 259 5 P91934 263 2 P91934 283 2 Q91128 294 2 Q95529 539 10 Q9M2B7 595 2 Q9RJ38 668 12 Q9EMQ2 1857 5 Q9VLH3 98 9 Q48436 197 2 Q52607 230 12 Q64748	100000000
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ALIGNMENTS

Gaps .	
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DRELIMINARY; PRT; 301 AA. 50 EB-1997 (TrEMBLrel. 02, Last sequence update) EB-1997 (TrEMBLrel. 10, Last sequence update) UN-2001 (TREMBLrel. 17, Last annotation update) PHATIDYLSERINE DECARBOXYLASE (EC 4.1.1.65). mydia trachomatis. eria; Chlamydiales; Chlamydiaceae; ChlamydiaTaxID-813; ENCE FROM N.A. INTH-LZ/434 ABU; arty G.A.; itted (SEP-1996) to the EMBL/GenBank/DDBJ databases. CATALYTIC ACTIVITY: PHOSPHATIDYL-L-SERINE = PHOSPHATIDYLETHANOLAMINE + CO(2). CORACTOR: PXRIDOXAL-PHOSPHATE OR PYRUVATE. PHOSPHATIDYLETHANOLAMINE + CO(2). CORACTOR: PXRIDOXAL-PHOSPHATE OR PYRUVATE. FPO: 1PR003817; PS_DCarbxylase. PRO015; AAB17564.1; - ENCE 301 AA; 34064 MW; A4E852492F408207 CRC64; atch 90.0%; Score 27; DB 2; Length 301; cal Similarity 85.7%; Pred. NO. 56; 6; Conservative 1; Mismatches 0; Indels SMAIARL 7 : SMAIARL 164	T 2 084705 PRELIMINARY; PRT; 301 AA. 084705, 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
SULT 7850 P778 P778 O1-F 01-F 01-F 01-F 01-F 01-F 01-J 01-F 01-J 01-J 01-J 01-J 01-J 01-J 01-J 01-J	ULT 705 08 08 01
RESULT P77850 D10 P P77850 D11 P P77850 D11 P P P77850 D12 P P P P P P P P P P P P P P P P P P P	RESULT 084705 ID 0 AC 0 DT 0 DT 0

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Dioxygenase
SEQUENCE
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Q9C6F0;
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STARIN-MODN / NIGG:
MEDLINE-20150255; Pubbed-10684935;
REad T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumonlae.AR39.";
                                                                                     STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                          Genome sequence of an obligate intracellular pathogen of humans:
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0
                                                                                                                                                                                                                                                   Length 301;
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Pred. No. 56;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                    301 AA; 34076 MW; D82A7E0272CCC896 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09E427CA5CD5ACF2 CRC64;
01-JUN-2001 (TremBlrel. 17, Last annotation update)
PHOSPHATIDYLSERINE DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHATIDYLSERINE DECARBOXYLASE PROENIYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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56;
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                                                                                                                                                                                                                                                   Score 27;
Pred. No. 5
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EMBL; AE002274; AAF38954.1; -.
TIGR; TC0072; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003817; PS_Dcarbxylase. Pfam; PF02666; PS_Dcarbxylase; 1.
                                                                                                                                                                                    InterPro; IPR003817; PS_Dcarbxylase.
Pfam; PF02666; PS_Dcarbxylase; 1.
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                              Science 282:754-759(1998).
EMBL; AE001340; AAC68294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34113 MW;
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85.7%;
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85.7%;
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Best Local Similarity 85...
5. Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                       Chlamydia trachomatis.
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         Complete proteome.
SEQUENCE 301 AA:
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| 158 SMAIARL 164
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158 SMAIARL 164
                                                       NCBI_TaxID=813;
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                      PSDD OR CT699
                                                                                                                                 Davis R.W.
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09PLM7
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REALINE—21016719; PubMed=11130712;

REDLINE—21016719; PubMed=11130712;

REDLINE—21016719; PubMed=11130712;

REDLINE—21016719; PubMed=11130712;

RA Theologia A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Ra Chung M.K., Conn L., Chan T.V., Feng J.-D., Fong B., Fulii C.Y.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Langin Hooper S., Lee A., Lee J.M., Lenz C.B., Kan A., Lam B.,

RA Langin Hooper S., Lie A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Langer B. L., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Langer B. L., Van Aken S., Waysberg M., Robat B.,

"Langer B. L., Van Aken S., Waysberg M., Robat B.,

"Langer B., Van Aken S., Waysberg M., Robat B.,

"Langer B., Van Aken S., Waysberg M., Robat B.,

"Langer B., Waller J.C., Davis R.W.;

"Langer B., Waller J.C., Davis R.W.;
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                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Monfort A., Casacuberta E., Puigdomenech P., Hoheisel J.,
Mewes H.W., Mayer K.F.X., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYOSCYAMINE 6-DIOXYGENASE HYDROXYLASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 42.7 KDA PROTEIN.
T19P19.150 OR AT4G39760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408 816-820(2000).

EMBL, AC079605, AAG50602.1; -.
InterPro; IPR002419; Fe_asc_oxidored.
InterPro; IPR002283; IPN_synth.
Pfam; PF00671; Fe_Asc_oxidored; 1.
PRINTS; PR00682; IPNSYNTHASE.
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Similarity 85.7%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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us-09-765-086-207.rspt

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307 AA.
                                                                                                                                                                                                                                            MEDLINE=97404404; PubMed=9256491;
                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002606; FAD_Synth.
Pfam; PF01687; FAD_Synth; 1.
ProDom; PD003662; FAD_Synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.78;
71.48;
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Best Local Similarity 71.4°,
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                  PRELIMINARY;
                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-SB1003;
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205 NMSVARL 211
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                                                                                                                                                          Rhodobacter
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                                  068069;
                  068069
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Q9CSE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99310339; PubMed-10382966; Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nanqai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kubilda N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                              SEQUENCE FROM N.A.
Monfort A., Casacuberta E., Pulgdomenech P., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 10; Length 369;
Pred. No. 68;
2; Mismatches 0; Indels
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Pred. No. 1e+02;
2; Mismatches 0; Indels
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01-NoV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
305Aa LONG HYPOTHETICAL DIDP-4-DEHYDRORHAMNOSE REDUCTASE.
                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL012605; CAA18762.1; -.
EMBL; AL161595; CAB80639.1; -.
Mendel, 29837; Arath; 3427; 29837.
InterPro; IPRO01810; F-box.
InterPro; IPR001798; Kelch.
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                   al protein.
369 AA; 42660 MW; 900E2D1C01539684 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP000061; BAA80165.1; -.
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SEQUENCE 305 AA; 34301 MW;
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71.4%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                       Pfam: PF00646; F-box; 1.
Pfam: PF01344; Kelch; 1.
SMART; SM00256; FB0X; 1.
PROSITE; PS50181; FB0X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
'... 5; Conserve
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                                                                                                                      SEQUENCE FROM N.A.
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|162 SMSVARI 168
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SMTVARL 105
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RESULT

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C STRAIN-C57BL/G5. TISSUB-EMBRYO;

KX MEDLINE-2108560; PubMed=11217851;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa H.A., Ashburner M., Batalov S., Casavant T.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Achin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochin P., Loyin B., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nymshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymshav-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                             Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189 kb segment of the chromosome of Rhodobacter capsulatus SB1003."; Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

EMBL; AF010496; AAC16155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 33.2 KDA PROTEIN.
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria, Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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307 AA; 33190 MW; 33CDFFED0FBFD6F6 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2810417D08RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA.
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Gaps

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090417; 090417 6

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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3954899) (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                    Score 26; DB 4; Length 571;
Pred. No. 1.9e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 3; Length 849; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                              SEQUENCE FROM N.A.
TISSUE-SKIM, AND MELANOMA;
Strausberg H. Strausberg S. Strausberg S. Strausberg S. Strausberg S. Strausberg S. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC002929; AAH02929.1; -.
SEQUENCE 571 AA; 63247 MW; A1E7188792D7AE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urrestarazu L.A.,
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andre B., Urrestarazu L.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X94607; CAA64304.1; --
EMBL, Z73229; CAA97587.1; --
EMBL, Z73229; CAA97589.1; --
SGD, S0000407; YLR057W.
InterPro; IPR001382; Glyco_hydro_47.
Pfam; PPE01522; Glyco_hydro_47.
Probom; PRO03239; Glyco_hydro_47; 1.
SEQUENCE 849 AA, 96996 MW; A6B87AC32936AOD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                        86.7%; SCUL.
71.4%; Pred. NO. 1...
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1204 AA.
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4*
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Best Local Similarity
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SEQUENCE FROM N.A.
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| SMSLARI 525
                                                                                              NCBI_TaxID=9606;
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MEDLINE-96009547; PubMed-7565671;
Jones B.B., Ohno C.K., Allenby G., Boffa M.B., Levin A.A.,
Grippo J.F., Petkoyich M.;
"New retinoid X receptor subtypes in zebra fish (Danio rerio)
differentially modulate transcription and do not bind 9-cis retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                        Gaps
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes: Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid.";
Mol. Cell. Biol. 15:5226-5234(1995).
1- SUBLELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
HSSP; P19793; ZNLL.
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                                                                                                          Score 26; DB 11; Length 317;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
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EMBL; AK013101; BAB28647.1; -.
MGD; MGI:1917672; 2810417D08R1K.
1 1 1
SEQUENCE 317 AA; 34869 WW; 7D99ADD59C36BC82 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RETINOID X RECEPTOR DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                            422 AA
                                                                                                                                                    2; Mismatches
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InterPro; IPRO00536; Hormone_rec_lig.
InterPro; IPRO01723; Strdhormone_receptor.
InterPro; IPRO01628; zf-C4.
Pfam: PP00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
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PRINTS; PRO0047; STROIDFINGER.
SMART; SMO0430; HOLI; 1.
SMART; SMO0430; HOLI; 1.
PROSITE; PSO0031; NUCLEAR_RECEPTOR; 1.
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                                                                                                              Query Match 86.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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186 SLSVARL 192
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Q9BU29;
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RESULT 10

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09BU29 ID 09 AC 05 DT 01

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Arabidopsis thaliana
                                                                               NCBI_TaxID=3702;
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Q85057;
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085057
AC 085057
DT 01-NOV
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                                                                                                                                                                                                                                               Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL136800; CAB66734.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN;
MEDILINE-20039619; PubMed-10574462;
MEDILINE-20039619; PubMed-10574462;
MEDILINE-20039619.

"Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4e+02;
2; Mismatches 0; Indels
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Pred. No. 4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 50B87F6FFF2A1088 CRC64;
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09SY14;
01-MAY-2000 (TYEMBLEGL. 13, Created)
01-MAY-2000 (TYEMBLEGL. 13, Last sequence update)
01-JUN-2001 (TYEMBLEGL. 17, Last annotation update)
11/POTHETICAL 134.3 KDA PROTEIN.
            01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 134.3 KDA PROTEIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1209 AA.
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                           1204 AA; 134345 MW;
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EMBL; AB033113; BAA86601.1; -.
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01-MAY-2000 (TrEMBLrel. 13, 1
KIAA1287 PROTEIN (FRAGMENT).
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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1073 SLSVARL 1079
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                                                                               DKFZP434H1220.
                                                                                                                                                                                                                              FISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 12
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Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mawes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                     Huang E.N., Nascimento L., de la Bastide M., Habermann K., Vil M.D., Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schutz K., Parnell L.D., Dedhian N.N., McCombie W.R.; R.R., "Arabidopsis thaliana BAC 77811 from chromosome IV near 10 cM."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cassidy B., Sherwood J.L., Nelson R.S.; "Cloning of the capsid protein gene from a blotch isolate of peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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Gunasinghe U.B., Flasinski S., Nelson R.S., Cassidy B.G.;
"Nucleotide sequence and genome organization of peanut stripe
potyvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 26; DB 10; Length 1216;
llarity 71.4%; Pred. No. 4.1e+02;
Conservative 2; Mismatches 0; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC007138; AAD22648.1; -
EMBL, AL161493; CAB80679.1; -
InterPro; IPR001680; WD40.
R Fām; PP00400; WD40; 7.
SMART; SM00320; WD40; 7.
R PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_3.
R PROSITE; PS50982; WD_REPEATS_2; 1.
R PROSITE; PS5094; WD_REPEATS_2; 1.
R PROSITE; PS5094; WD_REPEATS_REGION; 1.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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MEDLINE=93168029; PubMed=7916587;
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Arch. Virol. 128:287-297(1993)
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STRAIN-CV. COLUMBIA;
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NCBI_TaxID=28353;
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                                                                                                                       C STRAIN=BLOTCH;
A Gunsainghe U.B.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
C -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
DR EMBL, U05771; AAB01025.1; -.
DR MEROPS; C06.001; -.
DR MEROPS; S10.001; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001430; Peptidase_C4.
InterPro; IPR001456; Peptidase_C6.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001592; Poty_coat.
DR InterPro; IPR001264; Trypsin.
DR InterPro; IPR001205; RNA_POL_P3D.
InterPro; IPR001205; RNA_POL_P3D.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00869; Peptidase_C4; 1.
DR Pfam; PF00869; RNA_dep_RNA_POL; 1.
DR Pfam; PR00167; Poty_Coat.
DR Pfam; PR00167; Poty_Coat.
DR Pfam; PR001690; NIAPOTYPTASE.
DR SWART; SM00480; HELICC; 1.
DR PROSITE; PS00599; AA_TRANSFER CLASS_2; UNKNOWN_1.
FT CHAIN 444 900 HELICA:
FT CHAIN
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1300 1933 CI.

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2177 2419 NIA-VPG.

2420 2935 NIB.

3222 AA; 365723 MW; 96E3CE717D634B50 CRC64;
J. Gen. Virol. 75:2519-2525(1994).
[3]
                                                                                     SEQUENCE FROM N.A.
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Search completed: May 8, 2002, 07:20:16 Job time: 144 sec

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GenCore version 4.5 . Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May Run on:

8, 2002, 07:20:33 ; Search time 12.86 Seconds (without alignments) 19.958 Million cell updates/sec

US-09-765-086-207 30 1 SMSIARL 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	P56346 chlorella v	Q9mum5 mesostigma	-	Ξ	P77439 escherichia	P02369 escherichia	P51295 porphyra pu	P26161 rhodobacter	P18661 synechococc	-	P44996 haemophilus		P42786 neisseria g	Q9juv1 neisseria m	Q9jzr6 neisseria m	027262 methanobact				P32214 rattus norv	O51522 borrelia bu	P05353 agrobacteri	Q09263 caenorhabdi		-	٠.	Q04668 leishmania	Q01743 bacteriopha	P27009 octopus dof	P27014 octopus vul	Q25626 octopus vul	114	Q56301 thermococcu
SUMMARIES	dī	\vdash	MIND_MESVI	KHL1_HUMAN	KHL1_MOUSE	YPDD_ECOLI	RS13_ECOLI	RR13_PORPU	YPU5_RHOCA	RS7_SYNP6	ADH_DROPI	YIAJ_HAEIN	YYBE_BACSU	PIP_NEIGO	PIP_NEIMA	PIP_NEIMB	YB94_METTH	GSPF_XANCP	PS31_ARATH	PSD3_TOBAC	CALR_RAT	PYRG_BORBU	VIB4_AGRT9	YQD3_CAEEL	DPOM_PODAN	CHAO_DROME	RPB1_SCHPO	KPYK_LEIBR	DPA6_BPR69	SC1_OCTDO	SC2_OCTVU		YLP4_ZYMMO	KPYK_THELI
	Length DB	282 1	286 1	748 1	751 1	831 1	117 1	126 1	214 1	156 1	253 1	268 1	278 1	310 1	310 1	310 1	331 1	390 1	488 1	488 1	516 1	533 1	789 1	859 1	1197 1	1315 1	1752 1	91 1	187 1	215 1	215 1	215 1	_	220 1
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Gaps ; 0

Query Match 86.7%; Score 26; DB 1; Length 282; Best Local Similarity 100.0%; Pred. No. 14; Matches 6; Conservative 0; Mismatches 0; Indels

2 MSIARL 7 |||||| 39 MSIARL 44

οy qq RESULT 2 MIND_MESVI

053345 mycobacteri P13714 bacillus su Q18079 caenorhabdi Q96186 pecten maxi P72811 synechocyst O28105 archaeoglob P33770 rhodobacter 067259 aquifex aeo Q9383 eubacterium Q52964 rhizobium m P40066 saccharomyc		uo. ouxiophyceae; Chlorellales;	M., Ito M., Ito S., Suzuki Y., Hamada A., Ohta T., oroplast genome from the ence of genes possibly 72(1997). RRECT PLACEMENT OF THE LY, MIND SUBFAMILY.	a collabo MBL outsta Trictions is in n d for comm sib.ch/ann
NUDC_MYCTU LDH_BACSU YXTCAEEL NUIM_PECMA YGS9_SYNY3 YL78_ARCFU HEMF_RHOSH THIC_AQUAE SELA_EUBAC MOTD_RHIME FKHL_YEAST	ALIGNMENTS D; PRT; 282 AA. Created) Last sequence update) Last annotation update)	PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND. Chlorella vulgaris. Chloroplast. Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chloralaceae; Chlorella. NCBL_TAXID=3077; [1] SEQUENCE FROM N.A.	Sugita ki T., the chl e exist ", 5967-59 THE CO	the Swiss Institute of Bioinformatics and the swiss Institute of Bioinformatics and the son Bioinformatics Institute. There are no non-profit institutions as long as its cont and this statement is not removed. Usage by requires a license agreement (See http://www.nemail to license@isb-sib.ch). IPRO00707; ParA. 10991; ParA; 1. 1282 AA; 31013 MW; 94010DD45AE4AEC7 CRC64;
76.7 313 1 76.7 320 1 76.7 321 1 76.7 324 1 76.7 392 1 76.7 452 1 76.7 467 1 76.7 445 1 76.7 467 1 76.7 499 1	STANDARD; (Rel. 36, Created) (Rel. 36, Last seq (Rel. 40, Last ann	MIND. Chlorella vulgaris. Chloroplast. Eukaryota; Viridiplantae; C Choroplase. Choroplast. Sukaryota; Viridiplantae; C Chorellaceae; Chlorella. NCBL_TAXID=3077; SEQUENCE FROM N.A.	STRAIN-IAM C-27 / TAMIYA; MEDLINE-97303241; PubMed-9159184; MEDLINE-97303241; PubMed-9159184; Tsudzuki J., Nakashima K., Tsudzuki T., Inamura A., Yoshinaga K., Sugiura M.; "Complete nucleotide sequence of the chi green alga Chlorella vulgaris: the exist involved in chloroplast division."; Proc. NATL. Acad. Sci. U.S.A. 94:5967-55 -1- FUNCTION: ATPASE REQUIRED FOR THE CC DIVISION SITE (BY SIMILARITY).	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bioinformatics Institute of Bioinfuse by non-profit institutions as lamodified and this statement is not rementities requires a license agreement or send an email to licenseélab-sib. Chem. EMBL, ABOOI684, BAA57951.1;
2432100087654 24321000833333	LT 1 CHLVU MIND_CHLVU P56346; 15-JUL-1998 (15-JUL-1998 (20-AUG-2001 (PUTATIVE SEPTOM SITE-DET MIND. Chlorella vulgaris. Chloroplast. Eukaryota; Viridiplantae Chlorellaceae; Chlorella NCBI_TAXID=3077; [1]	STRAIN-IAM C-27 MEDLINE-973324 Wakasugi T., Na Tsudzuki J., Na Tsudzuki J., Na Inamura A., Yos Inamura A., Yos Inomura A., Yos	This SWISS-PROT entry is between the Swiss Institute European Bioinformatiuse by non-profit institutes by non-profit instituties requires a licerentities requires a licerentities, ABOO1684; BAA57951 InterPro; IPR000707; Park PFO0991; Park, 1. Cell division; Septation; NP_BIND 24 31013
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Q9JI74;
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KHL1_MOUSE
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MEDLINE=20150907; PubMed=10688199;
Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-1- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
                                                                                                                                                                    Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
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Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA8 transcript is an antisense RNA to a brain-specific
transcript encoding a novel actin-binding protein (KLHLI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.7%; Score 26; DB 1; Length 286; 100.0%; Pred. No. 14; 0; Indels tive 0; Mismatches 0; Indels
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25D8B8FB2258E3F9 CRC64;
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InterPro; IPR000707; ParA.
Pfam; PF00991; ParA; 1.
Cell division; Septation; ATP-binding; Chloroplast.
                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND
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  286 AA.
  PRT;
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MEDLINE=20277482; PubMed=10819331;
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Best Local Similarity 100.
Matches 6; Conservative
  STANDARD;
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                                                                                                                                                  Mesostigma viride.
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SEQUENCE
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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:143-150(2000).
                                                                                                                                                                                                Ray M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
THE BRAIN CELLS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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100.0%; Pred. No. 40;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                   -i-TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-i-SIMILARITY: CONTAINS I BTB/POZ DOMAIN.
-i-SIMILARITY: CONTAINS 6 KELCH REPEATS.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KELCH-LIKE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 AA
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SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF252279; AAF81716.1; -.
EMBL; AB040923; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC16128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20347694; PubMed-10888605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
SWART; SM0225; BTB; 1.
PROSTTE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF252283; AAF81719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82680 MW;
                                                                                                                                                                       SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000210; BTB_POZ.
InterPro; IPR001798; Kelch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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601
649
701
748 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 SMSIAR 590
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15
298
831 AA;
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Best Local Similarity
Matchès 6; Conserv
      SEQUENCE FROM N.A.
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757 SISIARL 763
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ID RS13_ECOLI
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Koob M.D., Nemes J.P., Benzow K.A.;
"The SCA0 transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHL1).";
Hum. Mol. Genet. 9:1543-1551(2000).
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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STRAIN-KIZ ' MG1652.
STRAIN-KIZ ' MG1652.
STRAIN-KIZ ' MG1657.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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30-MAY-2000 (Rel. 39, Last sequence update)
20-MOG-2001 (Rel. 40, Last annotation update)
PUTATIVE PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE YPDD
(EC 2.7.3.9) (PHOSPHOTRANSFERASE SYSTEM, ENZYME I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 26; DB 1; Length 751; 100.0%; Pred. No. 40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 5.
                                                                                              THE BRAIN CELLS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
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SER-RICH.
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InterPro; IPR000210; BTB_POZ.
InterPro; IPR001798; Kelch.
Pfam; PF00151; BTB; 1.
Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
SNART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Reper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463
510
558
604
652
704
751 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588 SMSIAR 593
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P77439;
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REPEAT
SEQUENCE
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REPEAT
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YPDD_ECOLI
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                                    A Tanamator V., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
A Tanamator V., Alba H., Baba T., Makino K., Miki T., Mitsuhashi N.,
A Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
A Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
Tanagata S., Horiuchi T.;
Tanagata S., Horiuchi T.;
Tanagata S., Horiuchi T.;
Takana G., Satoh Y., Satoh Mada C.,
Tanagata S., Horiuchi T.;
Takana S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tanagata S., Horiuchi T.;
Takana S., Saito N., Sampei G., Satoh Y., Uehara K., Wada C.,
Tanagata S., Horiuchi T.;
Takana S., Saito N., Sampei G., Satoh Y., Satoh Y., Wada C.,
Tanagata S., Horiuchi T.;
Tayana S., Saito N., Sampei G., Satoh Y., Satoh Y., Wada C.,
Tayana S., Saito N., Sampei G., Takemoto K., Uehara K., Wada C.,
Tayana S., Saito N., Sampei G., Satoh Y., Satoh Y.,
Tayani H., Takana C.,
Tayana S., Saito N., Sampei G., Satoh Y., Satoh Y.,
Tayani H., Takana S.,
Tayana S., Saito N., Sampei G., Satoh Y., Satoh Y.,
Takana C., Saita S., Wada C.,
Takana S., Saita S., Saita S., Saita S., Saita S., Saita S.,
Takana S., Saita 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00391; PEP-utilizers; 1.
Probom; PD000940; PEP_utilizers; 1.
Probom; PD001689; PTS_EIIA_2; 1.
PROSITE; PS00370; PEP_ENXYMES_PHOS_SITE; FALSE_NEG.
PROSITE; PS00742; PEP_ENXYMES_2; 1.
PROSITE; PS00369; PTS_HPR_HIS; PALSE_NEG.
PROSITE; PS00589; PTS_HPR_FISE_NEG.
Hypothetical protein; Phosphotransferase system; Transferase; Kinase;
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Escherichia.
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PHOSPHORYLATION (BY SIMILARITY).
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P02369;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-JUC-2001 (Rel. 40, Last annotation update)
30S RIBOSOMAL PROTEIN S13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME 1 DOMAIN.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIIA DOMAIN.
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MEDLINE=97349980; PubMed=9205837;
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ilarity 85.7%;
Conservative 1
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SEQUENCE FROM N.A.
MEDLINE-85242076; PubMed-2989779;
Bedwell D.M., Davis G.R., Gosink M., Post L.E., Nomura M., Restler H.,
Zengel J.M., Lindahl L.;
"Nucleotide sequence of the alpha ribosomal protein operon of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-35 FROM N.A.
MEDLINE-6202589; Pubmed-6793240;
Miura A., Krueger J.H., Itoh S., de Boer H.A., Nomura M.;
"Growth-rate-dependent regulation of ribosome synthesis in E. coli:
expression of the lacz and galk genes fused to ribosomal promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASS SPECTROMETRY.

MEDLINE=99196679; PubMed=10094780;

Arnold R.J., Reilly J.P.;

Arnold R.J., Reilly J.P.;

Annold Recharichia coli ribosomal proteins and their
posttranslational modifications by mass spectrometry.";

Anal. Biochem. 269:105-112(1999).

-: FONCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
INITIATION OF TRANSLATION.

-: MASS SPECTROMETRY: MW-12968.1; METHOD=MALDI.

-: SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                   for the alpha ribosomal protein
                                                                                                                                                           Perna N.T., Burland V.,
                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIJINE-97426617; VARABE-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.
                                                                                                                                                                                                                                                                                                    Lindemann H., Wittmann-Liebold B.;
Primary structure of protein S13 from the small subunit of
Escherichia coli ribosomes.";
Hoppe-Seyler's Z. Physiol. Chem. 358:843-863(1977).
                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12968 MW; 3277C328EBD0D3D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-35 FROM N.A.
MEDLINE-80182128; PubMed=6154696;
Post L.E., Arfsten A.E., Davis G.R., Nomura M.;
"DNA sequence of the promoter region for the alpoperon in Escherichia coli.";
J. Biol. Chem. 255:4653-4659(1980).
                                                                                      Nucleic Acids Res. 13:3891-3903(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001363; Ribosomal_S13; 1. PROSITE; PS00646; RIBOSOMAL_S13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoGene; EG10912; rpsM.
InterPro; IPR001892; Ribosomal_S13.
                                                                                                                                                                                                                                                                        STRAIN=K;
MEDLINE-77248097; PubMed-330375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M12432; AAA83903.1; -.
EMBL; U18997; AAA58093.1; -.
EMBL; AE000407; AAC76323.1; -.
EMBL; X02543; CAA26392.1; -.
EMBL; M10213; AAA72457.1; -.
PIR; A23807; R3EC13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00416; Ribosomal_S13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 25:773-782(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                        Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Mol. Biol. Rep. 13:333-335(1995).
--- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE INTITATION OF TRANSLATION (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
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                                                        Gaps
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Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
MYPOTHETICAL 23.7 Kap PROTEIN IN PUHA 5'REGION (ORF214) (PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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85.7%; Pred. No. 11;
Length 117;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AA; 14538 MW; D7C26927606FE12B CRC64;
  DB 1;
                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S13.
     Score 25; DB ]
Pred. No. 9.9;
                                                                                                                                                                                                                                                                         126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 AA.
                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendel, 10345; PORPU; rps13;1.
InterPro; IPR001892; Ribosomal_S13.
Probom; PP00416; Ribosomal_S13; 1.
Probom; PD001363; Ribosomal_S13; 1.
PROSITE; PS00646; RIBOSOMAL_S13; 1.
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83.3%;
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                                                        Conservative
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Best Local Similarity
Matches 6; Conserv
     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                    73 SMSIKRL 79
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ID YPUS_RHOCA
AC P26161;
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P51295;
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PIR; S04428; S04428.
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Best Local Similarity
Matches 5; Conserv
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24 SMMVARL 30
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  DR DR DR SO WENT
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"Genes for the ribosomal proteins S12 and S7 and elongation factors
EF-G and EF-Tu of the cyanobacterium, Anacystis nidulans: structural
homology between 165 rRNA mrNA.";
Mol. Gen. Genet. 216:25-30(1989).
--- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
                                                                                                                                                                                    MEDLINE-84259352; PubMed-6744416; Youvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.; Mucleotide and deduced polypeptide sequences of the photosynthetic reaction-center, B870 antenna, and flanking polypeptides from R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%; Score 25; DB 1; Length 214; 71.4%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                           Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photosynthesis; Hypothetical protein.
SEQUENCE 214 AA; 23658 MW; BC4B773AF6631FA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 211165; CAA77519.1; -.
EMBL; KOII183; -; NOT_ANNOTATED_CDS.
PIR; C17807; S17807.
PIR; C28988; C28988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89281486; PubMed-2499762;
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                                                                                                                                                                SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                    capsulata.";
Cell 37:949-957(1984).
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                                                                SEQUENCE FROM N.A.
                   WCBI_TaxID=1061;
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129 SMSLAKL 135
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P18661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila picticornis (Fruit fly) (Idiomyia picticornis).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                        Gaps
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-1- SUBUNIT: HOMODIMER.
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=91163323; PubMed=2002765;
Rowan R.G., Hunt J.A.;
"Rates of DNA change and phylogeny from the DNA sequences of the alcohol dehydrogenase gene for five closely related species of
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                                        Indels
HSSP; P22744; IHUS:
InterPro; IPRO00235; Ribosomal_S7.
Prem: PPO0177; Ribosomal_S7; 1.
ProDom; PD000817; Ribosomal_S7; 1.
PROSTTE; PS00052; RIBOSOMAL_S7; 1.
SRIBOSOMAL Profein; RRNA-binding7;
SEQUENCE 156 AA; 17734 MW; 240FE99581CADCCC CRC64;
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NAD (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                      DB 1;
25;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-CTT-1996 (Rel. 34, Last annotation update)
ALCOHOL DEHYDROGENASE (EC 1.1.1.1).
                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                      Score 24;
Pred. No.
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InterPro: IPR003193; Adh_Short_C.
InterPro: IPR000205; NAD_binding.
Pfam; PF00106; adh_Short; 1.
Pfam; PF00663; adh_Short_C; 1.
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PRINTS: PR01167; INSADHFAMILY.
PRINTS: PR01168; ALCDHDRGNASE.
PROSTTE: PR00161; ADH_SHORT; 1.
OXIGOTEGUCEASE; NAD.
INIT_MET 0 0 BY SIND 9 32 NAD.
ACT_SITE 150 150 BY SEQUENCE 253 AA; 27437 MW; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. Evol. 8:49-70(1991).
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                                                                                                                                                                                                                                                                      80.0%;
ilarity 71.4%;
Conservative
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PRT;

STANDARD;

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PIP_NEIGO
P42786;
 YYBE_BACSU
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=RD, KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MERLIAMANN R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback Tr., Hanna M.C., Nguyen D.T., Sauddek D.M., Brandon R.C., Ghin L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
REGULATORS. STRONG, TO E.COLI YIAJ.
                                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD002768; HTH_IC1R; 1.
SMART; SM00346; HTH_ICIR; 1.
PROSITE; PS01051; HTH_ICLR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 80.0%; Score 24; DB 1; Length 268; Best Local Similarity 85.7%; Pred. No. 45; Matches 6; Conservative 0; Mismatches 1; Indels
 DB 1; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 H-T-H MOTIF (POTENTIAL).
30580 MW; AAAF3080ED39EA14 CRC64;
                                                                                                                                                     YIAJ_HAEIN STANDARD; PRT; 268 AA. P44996; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 20-ANG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1032.
                           2; Mismatches
 Score 24;
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000285; HTH_ICLR.
Pfam; PF01614; ICLR; 1.
80.0%;
71.4%;
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                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 AA;
        Best_Local Similarity
Matches 5; Conserv
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                                                                                161 TMSIAKL 167
                                                                                                                                                                                                                                                                                  Haemophilus.
NCBI_TaxID=727;
                                                    1 SMSIARL 7
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 Query Match
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                                                                                                                                        YIAJ_HAEIN
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
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1-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last anotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
                                                                                                                                                                                                                                                                                                                                          Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin."; DNA Res. 1:1-14(1994).
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 85.7%; Pred. No. 47; 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 H-T-H MOTIF (BY SIMILARITY).
31406 MW; 0F7750102F0FC0F7 CRC64;
                                                                                                                                                       Bacteria, Firmicutes, Bacillus/Clostridium group,
Bacillus/Staphylococcus group; Bacillus.
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last Sequence update)
02-0GJ-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YYBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
STRAIN=MS11 / MSO1-1X;
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                                                                                                                                                                                                                                                                                              STRAIN=168;
MEDLINE=96051385; PubMed=7584024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Subtilist; BG10026; yybE.
InterPro; IPR000847; HTH_LysR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D26185; BAA05198.1; -. EMBL; Z99124; CAB16104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
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                                                                                                                                 Bacillus subtilis.
                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | ||||||
| 9 SRSIARL 25
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ACT_SITE
SEQUENCE
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIM-22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd idagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
   5
F
FUNCTION: HYDROLYSES PEPTIDES HAVING THE STRUCTURE PRO-Y-Z-YIELD FREE PROLINE. ALSO HYDROLYSES THE DIPEPTIDE PRO-GLY. CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
D0E7AEBA908A1AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          1; Length 310;
                                                                                                                                                                                                                                                                                               NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                  SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE)
                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S33
                                                                                                                                                                                                               InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_11p_thioest_actsite.
InterPro; IPR002410; Pro_amnoPTase.
                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB
Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                   Pfan; PF00561; abhydrolase; 1.
PRINTS; PR00793; PROAMNOPTASE.
Hydrolase; Aminopeptidase.
                                                                                                                                                                                                                                                                                                                                     34791 MW;
                                                                                                                                                                                          EMBL; Z25461; CAA80948.1; -.
                                                                                                                                                                                                                                                                                                                                                                       80.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 71.4 nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                   310 AA;
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                                                                                                                                                                                                       MEROPS; S33.001;
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ACT_SITE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-MC58 / SEROGROUP B;

MEDLINE-2010755; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:1809-1815(2000).
-!- FUNCTION: SPECIFICALLY CATALYZES THE REMOVAL OF N-TERMINAL PROLINE RESIDUES FROM PEPTIDES (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL AMINOPEPTIDASE)
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9F888B54135478A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 1;
                                                                                                                                                                                                                                            Interpro; IPR003089; AB_hydrolase.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR0000539; Epox_hydrlse.
InterPro; IPR000379; Est_lip_thiosst_actsite.
InterPro; IPR002410; Pro_amnopTase.
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                                                                                                                                                                                                           EMBL; AL162755; CAB84384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00561; abhydrolase; I. PRINTS; PR00111; ABHYDROLASE. PRINTS; PR00412; PEPOXHYDRASE. PRINTS; PR00793; PROAMNOPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34900 MW;
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ilarity 71.4%;
Conservative 2
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Best Local Similarity
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or send an email to license@isb-sib.ch).

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           EMBL; AE00244; AAF41334.1; ...

R TIGR; NMB0927; ...

R InterPro; IPR003089; AB_hydrolase.

InterPro; IPR000073; Abhydrolase.

R InterPro; IPR000073; Abhydrolase.

R InterPro; IPR000073; Epox_hydrlse.

R InterPro; IPR000310; Pro_amnoPTase.

R PRINTS; PR0011; ABHYDROLASE.

R PRINTS; PR0011; ABHYDROLASE.

R PRINTS; PR0011; ABHYDROLASE.

R PRINTS; PR0012; EpoXHYDRIASE.

R Hydrolase; Aminopeptidase; Complete proteome.

R ACT_SITE 260 BY SIMILARITY.

T ACT_SITE 260 BY SIMILARITY.

T ACT_SITE 287 287 PROTON DONOR (BY SIMILARITY).

T ACT_SITE 287 287 PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                          Query Match 80.0%; Score 24; DB 1; Length 310; Best Local Similarity 71.4%; Pred. No. 53; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       1 SMSIARL 7
| ::|||||
217 SLAIARL 223
qq
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Search completed: May 8, 2002, 07:20:34 Job time: 162 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Мау

Run on:

8, 2002, 07:19:31 ; Search time 22.68 Seconds (without alignments) 23.511 Million cell updates/sec

US-09-765-086-207 30 1 SMSIARL 7 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008

Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DNA processing cha	transcription regu	hypothetical prote	transcription regu	prolyl aminopeptid	probable prolyl am	proline iminopepti	hypothetical prote	hypothetical prote	acetylpolyamine am	hypothetical prote	xpsF protein - Xan	xpsF protein - Xan	calcitonin recepto	calcitonin recepto	protein 21D7 - com
E64561	865992	T32333	F82446	S39592	F81878	B81141	F72575	A83708	C69026	T01839	S17938	T12057	A37430	S33746	T02207
7	7	7	~	~	7	7	7	7	٦	7	П	7	~	~	7
270	278	299	301	310	310	310	313	318	331	336	390	390	478	479	488
80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 D81745 probable phosphatidylserine decarboxylase (EC 4.1.1.65) precursor TC0072 [similarity]
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000 C; Accession: D81745
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A:Reference number: A81500: MUID:20150255
A;Accession: D81745 A;Status: preliminary
A; Molecule type: DNA A; Residues: 1-301 <tet></tet>
A, Cross-references: GB:AE002275; GB:AE002160; NID:g7190108; PIDN:AAF38954.1; PID:g719 A, Experimental source: strain Nigg (MoPn)
C; Genetics:
C; Superfamily: Escherichia coli phosphatidylserine decarboxylase
C;Keywords: carbon-carbon Lyase; carboxy-Lyase
Query Match 90.0%; Score 27; DB 2; Length 301;
ive

||:|||| |158 SMAIARL 164 1 SMSIARL 7 δ q

~ RESULT

phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - Chlamydia trachomatis (ser C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: 13-569-1998 #sequence_revision 13-Sep-1998 #text_change 28-Jul-2000
C; Accession: E71482
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A; Tille: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A; Reference number: A71570; MUID:99000809

A. Accession: E71462
A. Status: preliminary
A. Status: preliminary
A. Molecule type: DNA
A. Molecule type: DNA
A. Conserved to the type: DNA
A. Cross-references: GB. AE001340; GB. AE001273; NID: g3329147; PIDN: AAC68294.1; PID: g332
A. Experimental source: serotype D, strain UW-3/Cx
A. Cenetics:
A. Gene: psdD
C, Superfamily: Escherichia coli phosphatidylserine decarboxylase
C, Keywords: carbon-carbon lyase; carboxy-lyase

a

162 SMSVARI 168

g

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cell division inhibitor - Chlorella vulgaris chloroplast
C; Species: chloroplast Chlorella vulgaris
C; Species: chloroplast Chlorella vulgaris
C; Species: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Accession: T07303
R; Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A; Title: Complete nucleotide sequence of the chloroplast genome from the green alga C A; Reference number: 215985; MUID:97303241
A; Accession: T07303
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mcleule type: DNA
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: G72588
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable dTDP-4-dehydrorhamnose reductase APE1179 - Aeropyrum pernix (strain K1)
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A;Residues: 1-305 <KAW>
A;Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BAA80165.1; PID:95104851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-282 <WAK>
A;Residues: 1-282 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57951.1; PID:g2224467
C;Genetics:
A;Gene: mind
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C;Species: Rhodobacter capsulatus
C;Species: Thodobacter capsulatus
C;Accession: T03502
R;Vicek, C;Pacess, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
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38;
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C, Superfamily: dTDP-dihydrostreptose synthase
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C;Superfamily: cell division inhibitor minD
C;Keywords: chloroplast
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Best Local Similarity
Matches 6; Conserv
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| 99 SMTVARL 105
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                                                                                                                                                                                                                                                                                                                                                                               probable hyoscyamine 6-dioxygenase hydroxylase [imported] - Arabidopsis thaliana c; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: G86472
C; Accession: G76472
C
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C;Genetics:
                                                                                 Gaps
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           Length 301;
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A;Molecule type: DNA
A;Residues: 1-369 <BEV>
A;Cross-references: EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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Pred. No. 24;
1; Mismatches
       DB 2;
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Pred. No. 27;
2; Mismatches
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A;Note: T19P19.150
C;Superfamily: caffeoyl-CoA 3-0-methyltransferase
   Score 27; DB 2
Pred. No. 22;
1; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Ouery Match
Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-329 <STO>
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| 150 SMAIARL 156
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| 158 SMAIARL 164
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Pred. No. 1.2e+02;
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757 SISIARL 763
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757 SISIARL 763
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C; Species: Brachydanio rerio (zebra fish)
C; Species: Brachydanio rerio (zebra fish)
C; Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 20-Sep-1999
C; Accession: 150516
R; Jones, B. B.; Ohno, C.K.; Allenby, G.; Boffa, M.B.; Levin, A.A.; Grippo, J.F.; Petkovic Mol. Cell. Biol. 15, 5226-5234, 1995
A; Title: New retinoid X receptor subtypes in zebra fish (Danio rerio) differentially mod A; Reference number: A57301; MUID:96009547
A; Accession: 150516
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-422 <JON>
A; Residues: 1-422 <JON>
A; Residues: 1-422 <JON>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: unassigned erbA-related proteins; erbA transforming protein homolow:
C; Keywords: zinc finger
F; 88-341/Domain: erbA transf
               A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003 A;Reference number: 214955; MUID:97404404 A;Reference number: 214955; MUID:97404404 A;Recension: T03502 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-307 <VLC> A;Residues: 1-307 <VLC> A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16155.1; PID:g3128303 C;Genetics: A;Map position: 1 C;Superfamily: conserved hypothetical protein HI0963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A85881

A85881

Appotherical protein 23648 [imported] - Escherichia coli (strain 0157:H7)

C;Species: Escherichia coli

C;Species: Escherichia coli

C;Species: Scherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C;Accession: A85881

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousls, K.; Apodaca, Arithe: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Molecule type: DNA
A;Residues: 1-831 <STO>
A;Cross-references: GB:AE005174; NID:912516757; PIDN:AAG57509.1; GSPDB:GN00145; UWGP:236
A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                       Length 307;
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0
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Pred. No. 41;
2; Mismatches
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71.4%; Pred. No. 58;
Live 2; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative :
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205 NMSVARL 211
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53 SMSVSRL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 SMSIARL 7
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Matches
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Cispecies: Escherichia coli

Ci) ate. 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999

C; Accession: D65012

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617

A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-831 <BLAT>
A; Residues: 1-831 <BLAT>
A; Cross-references: GB:AE000326; GB:U00096; NID:g1788718; PIDN:AAC75442.1; PID:g17887
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: phosphotransferase system enzyme I homology
F;118-670/Domain: phosphotransferase system enzyme I homology <PTI>
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A; Residues: 1-849 <AND>
A; Residues: 1-849 <AND>
A; Residues: 1-849 <AND>
C; Residues: 1-840 <AND
C; Resid
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N;Alternate names: hypothetical protein L2153
C;Species: Saccharomyces cerevisiae
C;Dapeide: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 21-Nov-1997
C;Accession: S61631; 864885
R;Urrestarazu, L.A.
submitted to the EMBL Data Library, December 1995
A;Reference number: S61618
A;Reference number: S61618
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A; Residues: 1-849 <URR>
A; Cross-references: EMBL:X94607; NID:g1181264; PID:e217771; PID:g1181278
A; Andre, B.; Urrestarazu, L.A.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64872
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ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0; Indels
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hypothetical protein b2383 - Escherichia coli (strain K-12)
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Pred. No. 1.2e+02;
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A. Experimental Source: strain K
R. Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Recence number: A64720; MUID:97426617
A;Accession: E65122
A;Status: nucleic acid sequence not shown; translation not shown
                 A;Cross-references: GB:X02543; NID:g42795; PIDN:CAA26392.1; PID:g581217
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Lindemann, H.; Wittmann-Liebold, B.
Hoppe-Seyler's Z. Physiol. Chem. 386, 843-863, 1977
A;Title: Primary structure of protein S13 from the small subunit of Escherichia coli
A;Reference number: A02731; MUID:77248097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 1;
Pred. No. 28;
0; Mismatches 1
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                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 2-118 <LIN>
  A; Molecule type: DNA
A; Residues: 1-118 <BED>
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A;Map position: 73 min
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74 SMSIKRL 80
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: 685926
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reture: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <STO>
A;Residues: 1-98 <STO>
A;Residues: 1-98 <STO
A;Residues: 1-98 <STO
A;Residues: 1-98 <STO
A;Resperimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
A;Genetics: 24077
                                                                                                                            hypothetical protein AT4901860 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: H85023
R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: H85023
A;Accession: H85023
A;Accession: H85023
A;Accession: H85023
A;Cross-references: GB:NC_001268; NID:97268570; PIDN:CAB80679.1; GSPDB:GN00140
A;Cross-references: GB:NC_001268; NID:97268570; PIDN:CAB80679.1; GSPDB:GN00140
A;Genetics: A74901860
A;Map position: 4
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: A23807; A02731; E65122
R;Bedwell, D.; Davis, G.; Gosink, M.; Post, L.; Nomura, M.; Kestler, H.; Zengel, J.M.; Nucleic Acids Res. 13, 3891-3903, 1985
A;Title: Nucleotide sequence of the alpha ribosomal protein operon of Escherichia coli.
A;Reference number: A23807; MUID:85242076
A;Accession: A23807
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Pred. No. 1.8e+02;
2; Mismatches 0;
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Pred. No. 23;
1; Mismatches
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71.4%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 5; Conserv
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601 SLSVARL 607
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SMSVAR 17
9
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  1 MSIARL
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R3EC13
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A,Molecule type: DNA
A,Residues: 1-118 <BLAT>
A;Cross-references: GB:AE000407; GB:U00096; NID:92367211; PIDN:AAC76323.1; PID:917896
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Start codon: GTG
C.Complex: the ribosome is composed of the large (50S) and small (30S) subunit; the l
S TRNA and 22 distinct proteins
C:Complex: small subunit ribosomal proteins: S1 (PIR:R3EC1), S2 (PIR:R3EC2), S3 (PIR:
R3EC10), S11 (PIR:R3EC11), S12 (PIR:R3EC12), S13 (PIR:R3EC13), S14 (PIR:R3EC14), S15
C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-118 <STO>

A; Coss-references: GB:AE005174; NID:912517927; PIDN:AAG58419.1; GSPDB:GN00145; UWGP:

A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
                                                                                                                                                          Riarnold, R.J.; Reilly, J.P.
Anal. Biochem. 269, 105-112, 1999
A;Title: Observation of Escherichia coli ribosomal proteins and their posttranslation
A;Reference number: A59071; MUID:99196679
                                                                                                                                                                                                                                                                                                                                                               acid la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30S ribosomal subunit protein S13 [imported] - Escherichia coli (strain O157:H7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                 A; Contents: annotation; mass spectrographic analysis
A; Note: mass spectrographic analysis of post-translational modifications; any C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: G85994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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C;Superfamily: Escherichia coli ribosomal protein S13
C;Keywords: protein biosynthesis; ribosome
F;2-118/Product: ribosomal protein S13 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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C; Superfamily: Escherichia coli ribosomal protein S13
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ó 0; Gaps Query Match
83.3%; Score 25; DB 2; Length 118;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels

Qy 1 SMSIARL 7 | | | | | | | | Db 74 SMSIKRL 80

Search completed: May 8, 2002, 07:19:33 Job time: 101 sec

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May 8, 2002, 07:17:52 ; Search time 35.89 Seconds (without alignments) 57.058 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          473505 segs, 146272329 residues
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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62
                                                                                                                                                                             Title:
Perfect score:
Sequence:
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* SPTREMBL_17:*

1: sp_archea:*
2: sp_barcteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:* sp_plant:* 10: 11: 12: 14:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q99xt3 streptococc	Q9v6r9 drosophila	Q9c7v6 arabidopsis	Q9jqq9 neisseria m		Q20191 caenorhabdi	P95826 streptococc	Q54839 streptococc	055246 streptococc		Q9pmr1 campylobact	Q55279 streptococc	033631 streptococc	Q55098 streptococc	Q54840 streptococc	Q55312 streptococc	Q00720 group g str	Q914n1 streptococc	Q9k5d4 campylobact
SUMMARIES	ΩI	099хт3	Q9V6R9	Q9C7V6	600160	09х1н8	Q20191	P95826	Q54839	055246	055278	Q9PMR1	Q55279	033631	Q55098	Q54840	055312	000720	Q9L4N1	Q9K5D4
	DB	7	S	10	~	7	ა	~	7	7	7	7	7	~	7	7	~	7	~	7
	Query Match Length DB	805	389	476	222	426	648	208	436	441	454	455	472	475	532	550	587	592	592	276
æ	Query Match	67.7	66.1	65.3	64.5	64.5	63.7	62.9	62.9	62.9	62.8	62.9	62.9	62.9	62.9	62.9	62.9	62.9	62.9	61.3
	Score	42	41	40.5	40	40	39.5	39	39	39	39	39	39	39	39	39	39	39	39	38
	Result No.	1	7	m	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19

009785 saccharomyc 009958 caenorhabdi 099710 schizosacch 09az19 bacteriopha 09gse7 dictyosteli 099787 acreopyrum p 048758 listeria mo 093548 caenorhabdi 095614 bacillus ha 09590 neisseria m 058728 methanococc 020873 methanococc 020873 saenorhabdi 09973 staphylococ 014236 schizosacch 09vxs2 drosophila 099vx2 drosophila 099vx3 drosophila 099vx3 drosophila 099vx3 terosophila 099vx3 terosophila 094vx3 terosophila 094vx3 terosophila 094vx3 terosophila 094vx3 terosophila 094vx3 terosophila 091q47 caenorhabdi 094vy3 plasmodium 077005 plasmodium 067003 aquifex aeo	
Q03785 Q09958 Q987U0 Q987U0 Q98CE7 Q987SE Q987SE Q997SE Q997SE Q907SE Q907SE Q901Q4 Q9	Q99XW9 Q9U1B6
88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	212
461 1844 105 105 107 1127 1127 1240 1240 1240 1138 1138 1198 1198 1198	249
www.r.r.r.r.r.r.r.r.r.r.r.r.r.r.r.r.r.r	- :-:
601 601 601 601 601 601 601 601	28
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	36 36
01022222222222222222222222222222222222	44

ALIGNMENTS

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	01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PUTATIVE PYRUVATE FORMATE-LYASE 2 (EC 2.3.1.54). PFLD OR SPYZO49.	lllus/Clost	SEQUENCE FROM N.A. STRAIN-SF370; MEDLINE-21192684; Pubmed=11296296; Ferretti J.J., McShan W.M., Ajdic D., Ferrimeaux C., Sezate S., Suvorov A.N., Qian Y., Jia H.G., Najar F.Z., Ren Q	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an MI strain of Str Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001) EMBL; AEO06625; AAK34714.1; Lyase; Pyruvate; Transferase; Acyltransferase; C EEQUENCE 805 AA; 90464 MW; 3C41F1686D761B6E	67.7%; Score 42; DB 64.3%; Pred. No. 2e+ ive 3; Mismatches	PRT;
805 AA.	Created) Last sequence update) Last annotation updat ASE 2 (EC 2.3.1.54).	ridium gr	J., Savic , Kenton ., Zhu H.	, McLaughlin R.; MJ strain of Streptoco 18:4658-4663(2001). cyltransferase; Complet 3C41F1686D761B6E CRC64;	Score 42; DB 2; Pred. No. 2e+02; ; Mismatches	389 AA.
	ate) pdate) 4).	Streptococcus pyogenes. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus. NCBI_TaxID=1314;	SEQUENCE FROM N.A. STRAIN-SF370; MEDLINE-21192684; PubMed=11296296; Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Ferretta J.S., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001). EMBL; AE006625; AAK34714.1; Lyase; Pyruvate; Transferase; Acyltransferase; Complete proteome. SEQUENCE 805 AA: 90464 MW; 3C41F1686D761B6E CRC64;	Length 805; 2; Indels	

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MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
Minte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Minte O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
M. Lounn E., Candanith A.D., Hass B., Ronsen N.F., Hughes B., Fujil C.Y.,
M. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,
M. Hunter J.L., Jenklins J., Johnson-Hopson C., Khan S., Khaykin E.,
M. Lin S.Y., Liu Z.A., Lee A., Lee J.M., Lear C.A., Li J.H., Li Y.-P.,
M. Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
M. Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
M. Johnson-Wall M., Nguyen M., Nguyen W., Ngerman W.C., Osborne B.I.,
M. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzerg S.L., Tambunga G., Toriumi M.J., Town C.D.,
M. D., Yu G., Fraser C.M., Voysberg M., Vysotskaia V.S., Walker M.,
M. D., Yu G., Fraser C.M., Vortex J.C., Davis R.W.;
M. D., Yu G., Fraser C.M., Vortex J.C., Davis R.W.;
M. Sillen D., Well M., Well M., Mallen D., M., Walker M., Mallen D., Yu G., Peresson D., Peresson D., Peresson D., Peresson D., Peresson D., Peresson D., Voysotskaia V.S., Walker M.,
M. D., Yu G., Fraser C.M., Vortex J.C., Davis R.W.;
M. D., Yu G., Fraser C.M., Vortex J.C., Davis R.W.;
M. D., Yu G., Fraser C.M., Vortex J.C., Davis R.W.;
M. D., Mallen D., Wallen D., Wallen D., Walker M., Mallen D., Wallen D., Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-OCT-2000 (TREMBLrel. 15, Last sequence update)
HYPOTHETICAL PROTEIN NMA1321 (BASEPLATE ASSEMBLY PROTEIN V, PUTATIVE).
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STRAIN=22491 / SEROCROUP A / SEROTYPE 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhil J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000).
EMBL; AC066689; AAG51716.1; -.
SEQUENCE 476 AA; 55488 MW; D11027732F9C277C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 40.5; DB 1
57.1%; Pred. No. 2e+02;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA.
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Neisseria meningitidis (serogroup B).
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MEDLINE-20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₩,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLA-----KLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.3
Best Local Similarity 57.1
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                             NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99J009
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RAMADALINE-20196606; Pubbmed=10731132;
RAMADALINE-20196606; Pubbmed=10731132;
RAMADALINE-20196606; Pubbmed=10731132;
RAMADALINE-20196606; Pubbmed=107. RAMADALINE-201960600;
RAMADALINE-2019606; Raxier Ec., Helt. G., Nelson C.R., Miklos G.L.G., Raxier Ec., Helt. G., Nelson C.R., Miklos G.L.G., Raxier Ec., Helt. G., Nelson C.R., Miklos G.L.G., Raxier Ec., Helt. G., Nelson C.R., Blazely B.M., Rayland A., Baxendale J., Bayraktaroglu L., Beasley E.M., Rayland A., Baxendale J., Bayraktaroglu L., Beasley E.M., Rayland A., Baxendale J., Bayraktaroglu L., Beasley E.M., Rayland A., Baxendale J., Bayraktaroglu L., Boakley E.M., Rayland R., Bouck J., Burman D.P., Blundari D., Boltshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Brottler P., Rayland R., Boakley S., Dahlke C., Davenport L.B., Davies P.M., Roherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.M., Roherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Burtis R.C., Gabriellan A.E., Garg N.S., Celbart W.M., Glasser K., Godek A., Gong F., Gorrez C., Ferrige S., Dunkov B.C., Dun P. Durbin K.J., Evarey D., Helman T.J., Well M. H., Ibegwan C., Alakinson J.M., Ralush F., Karpen G.H., Ke Z., Kennisson J.M., Ketchum K.A., Howland T.J., Well M. H., Ibegwan C., Alali M. H., Howlison J.M., Ralush F., Karpen G.H., Ke Z., Kennisson J.M., Rettells M., Murphy B., Murphy D.M., Nosheefi A., Rether C., Krayltz S., Kulp D., Lai Z., Rako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rether B., McIlaina N.W., Nobarty C., Morris J., Mosheefi A., Shen H., Ralush M., Murphy B., Murphy 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pherygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43265 MW; 01409135653619F0 CRC64;
01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-WAY-2000 (TrEMBLrel. 13, Last annotation update) CG13333 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9C7V6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BZIP TRANSCRIPTION FACTOR, PUTATIVE.
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339 KLAELAKRLSTLA 351
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Best Local Similarity
Matches 9; Conserv
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Length 476; Indels

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases. EMBL; Z69791; CAA93663.1; ... EMBL; Z69793; CAA93663.1; JOINED. EMBL; Z69793; CAA93676.1; ... EMBL; Z69793; CAA93676.1; ... EMBL; Z69793; CAA93676.1; HSSP; P28825; 11AF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 648 AA; 73405 MW; 1661914F3CEAC71E CRC64;
                                                                                      Created)
Last sequence update)
Last annotation update)
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Pred. No. 3.8e+02;
1; Mismatches 2;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003502; ShKT.
InterPro; IPR0030130; Zn_MTpeptdse.
Pfam; PF01400; Astacin; 1.
SMART; SM00254; ShKT; 1.
SMART; SM00235; ZnMC; 1.
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73.38;
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                                                         Q20191; Q21661;
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 73.3
Matches 11; Conservative
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                                     PRELIMINARY;
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                                                                                                                                                                                                                          Caenorhabditis elegans.
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Streptococcus pyogenes
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                                                                                                                                                                      F39D8.4 PROTEIN
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NON_TER 208
SEQUENCE 208
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Q20191; Q216(
01-NOV-1996
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P95826;
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Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBdy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Ulterback T.R., Khouri H., Oin H., Vamachlevan J.,
Salli J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Complete genome sequence of Nelsseria meningitidis serogroup B strain
MC58.",
Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGLENCY N. N. N. STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heldelberg J., Sutton G.G., Flastschmann R.D., Elsen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria from
Genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
ENBL, AE001797; AAD36535.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.5%; Score 40; DB 2; Length 222;
69.2%; Pred. No. 1.1e+02;
ive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                           11 protein, Complete proteome.
222 AA; 23251 MW; E0AFE240175C90DF CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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PROSITE; PS00453; FKBP_PPIASE_1; UNKNOMN_1.
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InterPro; IPR002819; HD.
InterPro; IPR003607; HDc.
Pfam; PF01966; HD; 1.
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                                                                                                                                                                                                                                                                           EMBL; AL162755; CAB84572.1; -. EMBL; AE002460; AAF41502.1; -.
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3 LSKLAKKTAQTAK 15
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260 KVAELAKKIAK 270
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Brandt E.R., Good M.F.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U66005; AAB40642.1;
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                                            Created)
Last sequence update)
Last annotation update)
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Pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1
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Pred. No. 1.5e+02;
208 AA
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75.0%;
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SEQUENCE FROM N.A.
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NCBI_TaxID=1306;
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                                                                                                                                                                                                                                                                                          STRAIN=C36;
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NON_TER
SEQUENCE
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SIGNAL
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Q55278;
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Q9PMR1
ID Q9PMR1
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DT 01-TINN
DT 01-TINN
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Q55278
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  Gaps
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Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
Streptococcus.
NCBL_FaxID=1306;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Pred. No. 3e+02;
2; Mismatches 1; Indels
 Indels
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Pfam; PF02370; M. 8.
PRINES, PRODUL5; GPSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                     436 AA.
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Mismatches
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Mol. Gen. Genet. 237:287-300(1993).
EMBL, x58179; CAA41168.1; -.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001895; M_repeat.
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MEDLINE=93204905; PubMed=8455563;
5;
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75.0%;
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                                                                                                     01-NOV-1996 (TrEMBLEEL 01,
01-NOV-1996 (TrEMBLEEL 01,
01-JUN-2001 (TrEMBLEEL 17,
M PROTEIN TYPE 52.
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Best Local Similarity 75.0
Conservative
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116 KLAKQAEELAKL 127
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                  1 KLAKLAKKLAKL 12
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                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1314;
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6
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Q55246;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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MEDLINE-94291620; PubMed-8020466;
Ben Nasr A., Wistedt A., Ringdahl U., Sjobring U.;
Streptokinase activates plasminogen bound to human group C and (
streptococci through M-like proteins.";
Eur. J. Blochem. 222:267-276(1994).
BHSB1, 232:2677; CAR8588.1; -.
HSSP; P03069; 1GCL.
InterPro; IPR001899; Gram_pos_anchor.
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                                                                                                                                                      62.9%; Score 39; DB 2; Length 441; 75.0%; pred. No. 3.1e+02; Live 2; Mismatches 1; Indels
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Pfam; PF02370; M; 7.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM-POS_ANCHORING; UNKNOWN_1.
Actin-biding; Transmembrane.
SEQUENCE 441 AA; 49868 MW; 33DF991E365D9455 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE FUMARATE LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) MLC36 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ben Nasr A., Wistedt A., Ringdahl U., Sjobring U.;
Eur. J. Biochem. 0:0-0(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02370; M; 9.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                  454 AA.
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                                                                                                                                                      Query Match 62.9
Best Local Similarity 75.0
Matches 9; Conservative
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Matches 9; Conservative
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454
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389 KLAKQAEELAKL 400
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349 KLAKQAEELAKL 360
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30 >4
454 4
454 AA;
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407 KLAKQAEELAKL 418

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Streptococcus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geyer A., Schmidt K.H.; "Genetic organisation of the M protein region in human isolates of group C and G streptococci: two\ types\ of\ multigene\ regulator-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 475;
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Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 2; Mismatches 1; Indels
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STRAIN=GROUP C, C74A (ATCC 1238);
Podbielski A., Melzer B.;
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; X60097; CAA42693.1; -.
HSSP; P03069; IGCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES-S.dysgalactiae subsp. equisimilis; STRAIN-25287;
MEDLINE-20123454; PubMed-10660058;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S. equisimilis; STRAIN=25287;
Geyer A., Schmidt K.H.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
M PROTEIN.
                                                                                                                                                                                                            01-JAN-1998 (TremBirel. 05, Last sequence update)
01-JUN-2001 (TremBirel. 17, Last annotation update)
M-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (mgrC) regions.;
Mol. Genet. 262:965-974(2000).
EMBL; X93464; CAA63750.1; -
EMBL; X93464; CAA63750.1; -
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR00345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
Pram; PR0015; GPOSANCHOR.
PROSITE; PS00015; GROSANCHOR.
Transmenbrane.
                                                                                                                                       475 AA.
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InterPro; IPR003345; M_repeat.
Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                          Created)
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                                                                                                                                                       033631;
01-JAN-1998 (TrEMBLrel. 05,
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383 KLAKQAEELAKL 394
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                                                                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=119602;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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033631
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SEQUENCE FROM N.A.

CETRAIN-NCTC 11168;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688.M., Feltwell T., Holroyd S.,

Magels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Mutchead S., Barrell B.G.;

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Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBI_TaxID=197;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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"Streptokinase activates plasminogen bound to human group C and G streptococci through M-like proteins.";
ENEL. 212678; CAA83589.1; -.
EMBL, 232678; CAA83589.1; -.
Enterpro; PRROUBS9; Gram_pos_anchor.
Interpro; IRROUBS9; Gram_pos_anchor.
Pfam; PF02370; M, 9.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; Length 455;
Pred. No. 3.2e+02;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 AA; 51371 MW; C77CA8638C84B08F CRC64;
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8DE0886B2F45FFC8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
MLG72 PRECURSOR.
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472 AA; 53968 MW;
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Best Local Similarity 64.3.
Best Local 9; Conservative
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131 ELKAIAKALAKLAK 144
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STRAIN-SENDENCE FROM N.A.

STRAIN-SENDENCY PE M55;
MEDLINE-95371690; PubMed=7643859;
MEDLINE-95371690; PubMed=7643859;
A BOYLE M.D.P., Weber-Heynemann J., Raeder R., Podbielski A.;
Characterization of a gene coding for a type IIo bacterial IgG-
Thinding proctein..;
Mol. Immunol. 32:669-678(1995).

EMBL; X72090; CAA50980.1; -.
IR PEMBL; X72090; CAA50980.1; -.
R Pfam; PF00746; Gram_pos_anchor.
R Pfam; PF00746; Gram_pos_anchor; 1.
R PRINTS; PR00015; GPOSANCHOR.
R PRINTS; PR0033; GRAM_POS_ANCHORING; UNKNOWN_1.
W Transmembrane.
SEQUENCE 550 AA; 61736 MW; 32894BFF9805181B CRC64;
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Bacillus/Clostridium group; Streptococcaceae; Streptococcus.

Streptococcus.

CGI_TaxID-1314;
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                                                                                                                                                                                                                                                                           Ouery Match 62.9%; Score 39; DB 2; Length 532; Best Local Similarity 75.0%; Pred. No. 3.7e+02; Matches 9; Conservative 2; Mismatches 1; Indels
Pfam; PF02370; M; B.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Transmembrane.
SEQUENCE 532 Aa; 60362 MW; 4Ala78B9D1122787 CRC64;
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Last annotation update)
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054840 01-NOV-1996 (TIEMBLIEL 01, CI
01-NOV-1996 (TIEMBLIEL 01, LA
01-JUN-2001 (TIEMBLIEL 17, LA
M PROTEIN.
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440 KLAKQAEELAKL 451
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054840
AC 054840;
DT 01-NOV-
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DE M PROTE
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OS STREPTC
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GenCore version 4.5
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OM protein - protein search, using sw model

8, 2002, 07:17:52; Search time 12.86 Seconds May Run on:

(without alignments)
39.915 Million cell updates/sec

US-09-765-086-200 62 Perfect score:

1 KLAKLAKKLAKLAK 14 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	homo sapten	esche								drosophila				haemophilus		escherichia		caenorhabdi	xenopus lae			mesembryant	petroselinu						epifagus vi		sulfolopus	mycoplasma	streptococc
	Description	P29375	P43674	P12379	P43718	P07796	P47153	058221	013416	969800	005783	049407	Q9pp70	013923	P44857	P06102	P07118	. P03041	Q20222	P06893	059303	09zju8	P93253	001781	P50248	P40368	P47520	P46307	Q93324	000383	P13887	76xn60	P75442	P50470
SUMMARIES	ID	RBB2_HUMAN	YCAL_ECOLI	M24_STRPY	ATPE_HAEIN	H1G_STRPU	YJ86_YEAST	Y811_METJA	ORC2_HUMAN	MST2_DROHY	HMGD_DROME	Y269_MYCGE	GSA_CAMJE	CORO_SCHPO	PLSB_HAEIN	NOT3_YEAST	SYV_ECOLI	RPC1_BPP22	FAB3_CAEEL	H1B_XENLA	RPOD_PYRHO	TRPC_HELPJ	SAHH_MESCR	SAHH_PETCR	SAHH_TOBAC	NU82_YEAST	SPOT_MYCGE	RR3_CHLEU	MANB_CAEEL	YCF1_EPIVI	POLN_RRVN	KTH1_SULSO	Y240_MYCPN	SPH_STRPY
	DB	1	-	-		-	Н	-	Н			-	٦	-	,	Н	ч		-	Н	٦	Н	-	Н	-	Н	-	Н	-	П	-	_	7	1
	Length	1722	254	539	142	217	279	439	577	1391	112	340	424	601	810	836	951	92	171	219	259	452	485	485	485	713	720	800	006	1738	2479	189	344	376
dР	Query	69.4	62.9	62.9	-	61.3	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	59.7	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	56.5	56.5	56.5
	Score	43	39	39	38	38	38	38	38	38	37	37	37	37	37	, 37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36	32	32	32
	Result No.	-	7	m	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Pfam; PF01388; ARID; 1.
Pfam; PF02373; JmJC; 1.
Pfam; PF02375; JmJN; 1.
Pfam; PF00628; PHD; 3.
SMART; SM00501; BRIGHT; 1.

Min, 100206, InterPro; IPR001606, ARID, InterPro; IPR003347; JmjC. InterPro; IPR003349; JmjN. InterPro; IPR001965; PHD.

PIR; S16954; S16954. MIM; 180202; -.

P13050 streptococc P30141 streptococc	P49054 streptococc P16947 streptococc	P50468 streptococc 004658 arabidopsis	P12782 triticum ae	P36100 saccharomyc P08089 streptococc	P35007 catharanthu	_	P02977 streptococc
ARP4_STRPY MRP4_STRPY	PAM_STRPY M49_STRPY	M21_STRPY Y412_ARATH	PGKH_WHEAT	TZEA_YEAST M6_STRPY	SAHH_CATRO	YABN_BACSU	M5_STRPY
11	пп		Н.		Н	Н	-
386 388	388 389	407	480	482	485	489	492
56.5	56.5 56.5	56.5	56.5	56.5 56.5	56.5	56.5	56.5
35 35	35 35	3 3	35	35.5	35	32	35
34 35	36 37	8 6 8 8	40	4 4 2 4 2	43	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE RETINOBLASTOMA PROTEIN.
-1- SUBCELLIDIAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: TO THE C-TERMINAL DOMAIN OF THE XE169 PROTEIN AND THE JUMONJI PROTEIN A
                                                                                                                                                                                                                                                                                     MEDLINE-94020841; PubMed-8414517; Fattaey A.R., Herlin K., Dembski M.S., Dyson N., Harlow E., Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff A., Defeo-Jones D., Jones R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1102-1569 FROM N.A.
MEDLINE-913142450, PubMed=187421;
MEDLINE-913142450, PubMed=187421;
Hanobir M.G., Huber H.E., Oliff A.;
"Clonding of cDNAs for cellular proteins that bind to the retinoblascoma gene product.";
Nature 352:251-254(1991).
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       'Characterization of the retinoblastoma binding proteins RBP1 and
                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-0201 (Rel. 40, Last annotation update)
RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).
                                                                                PRT; 1722 AA.
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S66431; AAB28544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 8:3149-3156(1993).
                                                                                STANDARD;
                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE-94020841; I
                                                                                  RBB2_HUMAN
                                                                RBB2_HUMAN
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ACT_SITE
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MEDLINE-97061202; PubMed-8905232;
MEDLINE-97061202; PubMed-8905232;
MEDLINE-97061202; PubMed-8905232;
MEDLINE-97061202; PubMed-8905232;
MEDLINE-97061202; PubMed-8905232;
Memoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motcomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97426617; PubMed-9278503;
Blattner F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fricke J., Neublard J., Kelln R.A., Pedersen S.,
"The cmk gene encoding cytidine monophosphate kinase is located in
the rpsA operon and is required for normal replication rate in
scherichia coli.";
J. Bacteriol. 177:517-523(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M48 (ZINC
METALLOPROTEASE). STRONG, TO E.COLI YGGG.
                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                            DB 1; Length 1722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
SMART; SM00545; JmjN; 1.
SMART; SM00249; PHD; 3.
Trans-acting factor; Nuclear protein.
CONFLICT 1563 1566 MISSING (IN REF. 2).
SEQUENCE 1722 AA; 195815 MW; RCFFR8A8BAE69A652 CRC64;
                                                                                                                    Indels
                                                                                                                                                                                                                                   YCAL_ECOLI STANDARD; PRT; 254 AA. P43674; P75840; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) PUTATIVE METALLOPROTEASE YCAL (EC 3.4.24.-).
                                                                                           Score 43; DB 1
Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95138007; Pubmed=7836281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 150-254 FROM N.A.
                                                                                           69.4%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-183 FROM N.A.
                                                                                        Query Match 69.4
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 3:137-155(1996).
                                                                                                                                                                      1552 KLNKLAKKLAK 1562
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K12 / MG1655;
                                                                                                                                            1 KLAKLAKKLAK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                 KCAL OR B0909
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (POTENTIAL).
ERAGHIRDIATASGK -> DVRNTSVIVSPLVSKSLSSLRWS
SASPL (IN REF. 3).
ADDF70D17E9D93A0 CRC64;
between the Swiss Institute of Bioinformatics and the EMBL outstati
the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUW A.R., Beachey E.H., Burdett V.;
"Molecular evolution of streptococcal M protein: cloning and nucleotide sequence of the type 24 M protein gene and relation to other genes of Streptococcus pyogenes.";
J. Bacteriol. 170:676-684(1988).
-- FONCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPE OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-1- SIMILARITY: TO OTHER M PROTEINS.
-1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (CATALYTIC) (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01435; Peptidase_M48; 1.
Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        539 AA.
                                                                                                                                                                                                                               EMBL; AE000193; AAC73995.1; ALT_INIT
                                                                                                                                                                                                                                                             EMBL; D90728; BAA35644.1; -..
EMBL; D90729; BAA35653.1; -.
EMBL; U31523; AAA81515.1; ALT_INIT.
EMBL; X82933; CAA58106.1; -..
MEROPS; M48.006; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001915; Peptidase_M48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Vaughn / Serotype M24;
MEDLINE=88115166; PubMed=3276665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M PROTEIN, SEROTYPE 24 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26740 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 62.9%;
Similarity 57.1%;
8; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             EcoGene; EG13133; ycaL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLAKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M24_STRPY
ID M24_STRPY
AC P12379;
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERSONAL STATE STA
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                                                                                                                                                                                                                                                                                                                                                                                                                          -2 (1 ALTERATION).
-3 (2 ALTERATIONS).
-4 (1 ALTERATIONS).
-5 (2 ALTERATIONS).
-6 (1NCOMPLETE).
7 X 35 AA TANDEM REPEATS, B-TYPE.
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
5.3 X 35 AA TANDEM REPEATS, A-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                         PRINTS; PRO0015; GPOSANCHOR.
PROSITE: PS00343; GRAM_POS_ANCHORING; 1.
Signal; Virulence; Cell wall; Transmembrane; Phagocytosis;
Duplication; Repeat; Antigen; Colled coil.
SIGNAL 1 42 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                            POTENTIAL.
M PROTEIN, SEROTYPE 24.
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B03EDF3AC1E6E9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 57;
2; Mismatches
                                                      PIK; AZ8549; AZ8549.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                          Pfam; PF00746; Gram_pos_anchor; 1. Pfam; PF02370; M; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 AA; 58804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%;
75.0%;
                        EMBL; M19031; AAA26874.1; -.
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Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.9
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 KLAKQAEELAKL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLAKLAKKLAKL 12
                                               PIR; A28549; A28549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPE_HAEIN
P43718;
                                                                                                                                                                                                                                                                                  CHAIN
DOMAIN
TRANSMEM.
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDILINE-8112742; PubMed=3031476; MEDILINE-8112742; PubMed=3031476; Knowles J.A., Lai Z.-C., Childs G.J.; "Isolation, characterization, and expression of the gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         late histone subtype H1-gamma of the sea urchin Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purpuratus.";
Mol. Cell. Biol. 7:478-485(1987).
-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLECOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Aydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA; 15591 MW; E5BBDE1DA34A9039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA
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HSSP: P02259; 1HST.
InterPro: IPR001386; Linker_histone.
InterPro; IPR003216; Linkerhist_N.
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                                                                                                                                                                                                                                                                                                                               InterPro; IPR001469; ATP-synt_DE.
Pfam; PF00401; ATP-synt_DE; 1.
ProDom; PD000944; ATP-synt_DE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.38;
                                                                                                                                                                                                                                                                       EMBL; U32730; AAC22136.1; -. HSSP; P00832; 1BSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M16033; AAA30059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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118 VAKLSKELAKL 128
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                             TIGR; HI0478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H1G_STRPU
P07796;
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                                                                                                                                                                      Bult C.J., White O., Olson G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Cerlandege A.R., Dougherty B.A., Tomb J.F., Addms M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Riomk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                             Science 273:1058-1073(1996).
-!- SIMILARITY: TO M.JANNASCHII MJ0077 AND SOME, TO E.COLI YIEM.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%; Score 38; DB 1; Length 439; 69.2%; Pred. No. 67;
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2F85F2B942C1CDFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96099401; PubMed=7502077;
Gavin K.A., Hiddaka M., Stillman B.D.;
"Conserved initiator proteins in eukaryotes.";
science 270:1667-1671(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORC2_HUMAN STANDARD; PRT; 577 AA. 013416; 013204; 16. 013404; 17. Created) 30-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ORCIGIN RECOGNITION COMPLEX SUBUNIT 2. ORCIG. ORCIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                   SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO02035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; UNKNOWN_1.
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67525; AAB98810.1; -.
                     Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.3
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
REVISIONS TO 41-42.
Hidaka M., Stillman B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||| |:| | |
| 111 KLAKLNKELKKFA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
DOMAIN 273 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 439 AA;
                                                                                                                                                                                                                                                                                                                                                                   jannaschii.
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                ProDom; PD000373; Linkerhist_N; 1.
SWART; SMO526; H15; 1.
Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
SEQUENCE 217 AA; 22658 WW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Rose M., Koetter P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fundi; Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_FaxID=4932;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 32.0 KDA PROTEIN IN NNF1-SFE24 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 279;
                                                                                                                                        Length 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6610293B38B7F2B5, CRC64;
                                                                                                                                      DB 1;
36;
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Pred. No. 45;
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ID Y811_METJA STANDARD; PRT; 439 AA.
AC QS8221.
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 00-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DF HYPOTHETICAL PROTEIN MJ0811.
                                                                                                                                                                                                                                                                                                                                                               279 AA.
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                                                                                                                                      Score 38;
Pred. No.
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Pfam; PF00538; linker_histone; 1
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                                                                                                                                      61.38;
71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.3%;
61.5%;
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                                                                                                                                                                                10; Conservative
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100
131
156
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261 KMIRIAKKLAKPA 273
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193
239
279 AA;
                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                               YJ86_YEAST
P47153;
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YJ86_YEAST
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melanogaster
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; NCBL_TaxID=7224;
                                                                                                                        FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL BEBLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN APP-DEPENDENT MANNER.
SUBJUNIT: ORC IS COMPOSED OF SIX SUBJUNITS (BY SIMILARITY).
SUBJUNIT: DELONGS TO THE ORC2 FAMILY.
                                    MEDLINE-96404011; PubMed-8808289; Takahara K., Bong M., Brevard R., Eddy R.L., Haley L.L., Sait S.J., Shows T.B., Hoffman G.G., Greenspan D.S.; "Mouse and human homologues of the yeast origin of replication recognition complex subunit ORC2 and chromosomal localization of the cognate human gene ORC2L."; Genomics 31:119-122(1996).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=95045538; PubMed=7957199;
Neesen J., Padmanabhan S., Buenemann H.;
Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axonome-associated protein family Dhmstl01 form extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-helical rods within the extremely elongated spermatozoa of Doscophila hydei.";
Eur. J. Blochem. 225:1089-1095(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: TESTIS. PRIMARY SPERMATOCYTES AND EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%; Score 38; DB 1; Length 577; llarity 72.7%; Pred. No. 85; Conservative 2; Mismatches 1; Indels
 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                       DF3F9C2CF147DA5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   I -> V (IN REF. 3).
T -> L (IN REF. 3).
I -> M (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AXONEME-ASSOCIATED PROTEIN MST101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1391 AA.
                                                                                                                                                                                                                                                                                                                                                                                     DNA replication; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        65971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MST101(2).
Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                               EMBL; U40268; AAC50326.2; -. EMBL; U27459; AAB33970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      131
236
392
Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
15 Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|||| :|||
105 KMAKLASELAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                      577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLAKLAKKLAK 11
                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        MIM; 601182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MST2_DROHY
Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SPERMATIDS.
DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN THE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CANTON-S;
MEDLINE=94(21387; PubMed=8414994;
MEDLINE=94(21387; PubMed=84144994;
Mer S.S., Churchill M.E.A., Searles M.A., Travers A.A.;
"dHMG-Z, a second HMG-1-related protein in Drosophila melanogaster.";
Nucleic Acids Res. 21:4369-4371(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; I
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMGD_DROME STANDARD; PRT; 112 AA. 005783; Q9W2D3; 01-FEB-1995 (Rel. 31, Created) 20-FEB-1995 (Rel. 31, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 45-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIGH MOBILITY GROUP PROTEIN D (HMG-D). HMGD OR CG17950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 12:1915-1923(1992).
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MEDLINE=92236564; PubMed=1373803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X73481; CAA51876.1; -. PIR; S34154; S34154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Conservative
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9

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Gaps

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3; Indels

2; Mismatches

14

1 KLAKLAKKLAKLAK

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Ouery Match Best Local Similarity 64.3%; Matches 9; Conservative

Score 37; DB 1; Length 112; Pred. No. 29;

protein; Chromosomal protein; DNA-binding; 3D-structure.

PDB; 1HWA; 31-UUL-94.
FlyBase; FBgn0004362; HmgD.
InterPro; IPR000910; HMG_12_box.
Ffam; PF00505; HMG_box; 1.
SMARY; SM00398; HMG; 1.

EMBL; M77023; AAA28609.1; -. EMBL; AE003455; AAF46759.1; PIR; A44382, A44382. PIR; S32724; S32724.

ASP/GLU-RICH (ACIDIC). 3F537CCFD62FEC9F CRC64;

12416 MW;

112

DNA_BIND DOMAIN SEQUENCE

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Bockva D., Botchan M.R., Bouck J., Brokstein P., Botshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Poster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Dodson K.J., Brownes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harrey D., Heinan T.J., Wenison J.A., Ketchum K.A., Howland T.J., Wei M.-H., Ibegwam C., Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Lei Y., Lei Y., Martei B., McIntosh T.C., Morris J., Moshrefi A., Mortudo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Shen H., Shon B.C., Siden Krämen G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shong K., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Weinstock G.M., Weissenbach J., Mann G. Bong X., Wang S.M., Weissenbach J.C., Rheng X., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho X., Smith H.O., Rheng C., The Globs R.A., Weinstock G.M., Weinston B., Sheng X.H., Mers E.W., Rubin G.M., Venter J.C.; Staplenger G., Staplenge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Travers A.A.;
"HMG-D is an architecture-specific protein that preferentially binds
to DNA containing the dipucleotide TG.";
EMBO J. 14:1264-1275(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ner S.S., Travers A.A.; "HMG-D, the Drosophila melanogaster homologue of HMG 1 protein, is associated with early embryonic chromatin in the absence of histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE-95237208; PubMed=7720717;
Churchill M.E.A., Jones D.N.M., Glaser T., Hefner H., Searles M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [6]

REGILATE BY NUMR OF 2-74.

MEDIJIE 95006330; PubMed-7922039;
Jones D.N.M., Searles M.A., Shaw G.L., Churchill M.E.A., Ner S.S.,
Keeler J., Travers A.A., Neuhaus D.;
Keeler J., Travers A.A., Neuhaus D.;
"The solution structure and dynamics of the DNA-binding domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE-94222028; PubMed-8168480;
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SETAINE-96026346; PubMed-7569993;

MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Flictchman J.L., Weidman J.F., Sandla K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucler T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 340 AA; 39662 MW; 3921FE1F81501CC4 CRC64;
                                                                                            MYCGE Sign...
Y269 MYCGE Sign...
O49407; Q49428;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
` **rc-2001 (Rel. 40, Last annotation update)
` **rc-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol, 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                              Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39706; AAC71491.1; -.
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33530 /
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing
                                                                                              Y269_MYCGE
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EMBL; X71138; CAA50468.1; -.

601 AA

PRT;

STANDARD;

CORO_SCHPO

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AMINOLEGULINATE.
-1- COFACTOR: PYRIDOXL PHOSPHATE.
-1- PATHWAY: PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY; SECOND STEP.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CYTOPLASHIC (POTEWTIAL).
-1- SUBCELLULAR LOCATION: CYTOPLASHIC (POTEWTIAL).
-1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRIDOXAL PHOSPHATE (BY SIMILARITY). 7811526A5AEDA57D CRC64;
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                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOWUTASE (EC 54.3.8) (GSA)
(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT).
Score 37; DB 1; Length 340;
Pred. No. 76;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 37; DB 1; Length 424; 72.7%; Pred. No. 92; 1ve 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan, PF00202; aminotran_3; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
Porphyrin biosynthesis; Isomerase; Pyridoxal phosphate;
                                                                                                                                                                                                                 424 AA.
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000954; Aminotran_3.
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 59.7%;
58.3%;
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8; Conservative
                                       Conservative
                                                                                                                                                                                                                 STANDARD;
                                                                                                 ||| ||| ||: |
271 AKLTKKIAEITK 282
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                                                                           3 AKLAKKLAKLAK 14
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Best Local Similarity
                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                HEML OR CJ0853
                                                                                                                                                                                                               GSA_CAMJE
Q9PP70;
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   Query Match
                                   Matches
                                                                                                                                                                                           GSA_CAMJE
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RESULT 13 CORO_SCHPO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                     Harris D., Squares R., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
--- SUBUNIT: BINDS TO F-ACTIN (BY SIMILARITY).
--- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
--- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-NGC-2001 (Rel. 40, Last annotation update)
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.15) (GPAT).
PLSB OR H10748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
231096AE76CADE4D CRC64;
                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; WD40; 3.

SMART; SM00320; WD40; 3.

PROSITE; PS00678; WD_REPEATS_1; 1.

PROSITE; PS50082; WD_REPEATS_2; 3.

R PROSITE; PS50294; WD_REPEATS_2; 3.

T REPEAT 132 172 WD 1.

FT REPEAT 174 213 WD 3.

FT REPEAT 220 260 WD 4.

FT REPEAT 220 260 WD 5.

FT REPEAT 220 260 WD 7.

COLLED COLL. (POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Pred. No. 1.2e+02;
                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CRNNIN-LIKE PROTEIN CRN1.
CRNI OR SPAC23C4.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                           Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99753; CAB16873.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         581 KIAOLEDKLAKLTE 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLAKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLSB_HAEIN
P44857;
                                                                                                                                                                                                                        STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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Riles L., Rowley N., Skelton J., Smith V.,

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Job time: 161 sec
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                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: ACYL-COA + GLYCEROL 3-PHOSPHATE = COA +
1-ACYL-GLYCEROL 3-PHOSPHATE.
-i- PATHWAY. DE NOVO PHOSPHOLIPID BIOSYNTHESIS; FIRST STEP. MAY ALSO
PATHWAY. THE REGULATION OF MEMBRANE BIOGENESIS.
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geognagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Barrall B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86312926; PubMed=3018676;
Ferguson J., Ho J.-Y., Peterson T.A., Reed S.I.;
Nucleotide sequence of the yeast cell division cycle start genes
CDC28, CDC36, CDC37, and CDC39, and a structural analysis of the
predicted products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                 Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.7%; Score 37; DB 1; Length 810; 63.6%; Pred. No. 1.6e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JU-MAY-2000 (Rel. 39, Last annotation update)
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                810 AA; 92774 MW; DB8564BC3E2C370D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 31, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 14:6681-6697(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-FEB-1995 (Rel. 31, Last sequal 30-MAX-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U32758; AAC22406.1; -. TIGR; HI0748; -.
                                                                                                                                                                               Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 63.6 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 KIAOKLARVAK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                influenzae Rd.
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P06102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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NOT3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                    Genes Dev. 8:525-537(1994).

-1- FUNCTION: NEGATIVELY REGULATES THE BASAL AND ACTIVATED TRANSCRIPTION OF MANY GENES. PREFERBWIALLY AFFECTS TC-TYPE TATA ELEMENT-DEPENDENT TRANSCRIPTION. COULD DIRECTLY OR INDIRECTLY INHIBITS COMPONENT(8) OF THE GENERAL TRANSCRIPTION MACHINERY.
-1- SUBGNIT: FORMS A COMPLEX THAT COMPRISE NOT1, NOT2, NOT3, NOT4 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CAUTION; WAS ORIGINALLY (REF.1) THOUGHT TO BE CDC29 (WHICH IS IN
                                                                                                                                             Collart M.A., Struhl K.; "NOT3, and NOT4 encode a global-negative "NOT1(CDC39), NOT2(CDC36), NOT3, and NOT4 encode a global-negative regulator of transcription that differentially affects TATA-element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n regulation; Repressor; Coiled coil.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETIETGKN (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 836;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69B76694FCC6846F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I -> N (IN REF. 1)
Y -> C (IN REF. 1)
KQLKQGKISV -> ETIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: TO YEAST NOT5.
                                                                                                                   MEDLINE-95011559; PubMed=7926748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z46861; CAA86913.1; -. EMBL; X04289; CAA27837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94402
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831
106
725
836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLAKLA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; C26372; C26372, SGD; S0001300; NOT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    836 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACT NOT1).
                                                                                                                                                                                                                          utilization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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8, 2002, 07:20:33 Search completed: May

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Мау Run on:

8, 2002, 07:17:52; Search time 22.68 Seconds (without alignments) 47.021 Million cell updates/sec

1 KLAKLAKKLAKLAK 14 US-09-765-086-200 62 Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	retinoblastoma bin	hypothetical prote	baseplate assembly	conserved hypothet	hypothetical prote	probable heat shoc	cmk protein precur	M protein precurso	plasminogen-bindin	probable fumarate	plasminogen-bindin	M protein - Strept	M24 protein precur	Fc gamma (1gG) rec	H+-transporting AT	histone H1-gamma,	probable membrane	hypothetical prote	probable membrane	hypothetical prote	coiled coil protei	sperm tail-specifi	high mobility grou	probable gastrin p	hypothetical prote	UDP-glucose 4-epim	surface protein an	probable rotamase	 GTP-binding protei
SUMMAKIES	QI	178879	B96667	D81122	D72252	T23864	F85616	D64830	S30284	S43556	D81284	S43554	S54871	A28549	JC1419	C64071	A26721	S57139	C64401	S54543	T15543	T41515	S51364	A44382	B72593	T21215	C84114	G64229	A81794	C64466
	DB	-	7	~	7	~	~	7	~	7	~	7	~	ď	ď	7	7	~	7	7	~	7	~	~	~	~	~	ď	~	7
	Length	1722	476	222	426	648	262	262	436	454	455	472	532	539	587	142	217	279	439	461	462	1184	1390	112	127	246	282	340	347	393
ď	Query Match	69.4	δ.	64.5	64.5		65.9	62.9	62.9	62.9	62.9	62.8	62.9	62.9	62.9	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	59.7
	Score	43	40.5	40	40	39.5	39	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37
	Result No.	7	7	٣	4	Ŋ	9		80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote glutamate-1-semial	hypothetical gtp-b coronin-like prote	hypothetical prote hypothetical prote	glycerol-3-phospha cell division cont	valinetRNA ligas	valine tRNA synthe	regulatory protein	trans-regulatory p	histone H1B - Afri	histone H1B - Afri	translation elonga	adenosylhomocystei
T16480 E81358	T39037 T38258	T27465 H75013	D64090 S49940	SYECVT	E86124	Z1BPC2	H70371	HSXL1B	151447	154251	T15035
7 7	0 0	7 7	~ ~	-	7	7	7		7	a	7
412	537 601	634 758	810 836	951	951	92	218	219	220	227	227
59.7	59.7 59.7	59.7 59.7	59.7	59.7	59.7	58.1	58.1	58.1	58.1	58.1	58.1
37	37	37	37	37	37	36	36	36	36	36	36
30 31	32 33	34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	178879
	retinoblastoma binding protein 2 - human
	C;Species: Homo sapiens (man)
	C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
	C; Accession: 178879; S16954
	R; Fattaey, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hano
	Oncogene 8, 3149-3156, 1993
	A, Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
	A; Reference number: I58383; MUID:94020841
	A;Accession: 178879
_	A;Status: preliminary; translated from GB/EMBL/DDBJ
_	A; Molecule type: mRNA
_	A; Residues: 1-1722 <fat></fat>
	A;Cross-references: GB:S66431; NID:g435777; PIDN:AAB28544.1; PID:g435778
_	R; Defeo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M
	Nature 352, 251-254, 1991
_	A, Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene
	A; Reference number: \$16953; MUID:91312450
	A; Accession: S16954
	A;Status: not compared with conceptual translation
	A; Molecule type: mRNA
	A; Residues: 1102-1562, 'KKK' < DEF>
_	C; Genetics:
	A;Gene: GDB:RBP2
_	A;Cross-references: GDB:119548; OMIM:180280
	A; Map position: 3q21-3qter
	C;Superfamily: human retinoblastoma binding protein 2
_	

Gaps ó Query Match
Best Local Similarity 90.9%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 1; Indels

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Db 1552 KLNKLAKKLAK 1562 1 KLAKLAKKLAK 11 ŏ

7 RESULT

hypothetical protein F15H21.20 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: B96667
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunner, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

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Gaps

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Length 426; Indels

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C; Species: Escherichia coli (C; Date: Becherichia coli (B; Derna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Return preliminary
A; Molecule type: DNA
A; Residues: 1-262 <STO>
                                                                               A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Recession: D7252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <ARNN
A;Residues: 1-426 <ARNN
C;Residues: 1-426 <ARNN
C;Residues: 1-426 <ARNN
C;Genetics: Strain MSB8
C;Genetics:
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable heat shock protein ycaL [imported] - Escherichia coli (strain 0157:H7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 22/2; 112/3; 160/1; 250/1; 334/1; 424/3; 463/1; 485/3; 528/2; 593/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:269793; PIDN:CAA93676.1; GSPDB:GN00028; CESP:F39D8.4 A;Experimental source: clone R03A10 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F39D8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accesion: T23864
R;Hembry, C.
Submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.5; DB 2;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
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73.3%;
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Best Local Similarity 73.3
Matches 11; Conservative
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376 KLAKLGOKLGKTLAK 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z19809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:||||:||
260 KVAELAKKIAK 270
                                                             Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLAKLAKKLAK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-648 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:F39D8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T23864
                                                                                                                                                                                                                                                                                                                                                                A; Gene: TM1467
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A.Residues: 1-22 < TETS.
A.Crossidues: 1-22 < TETS.
A.Experimental source: serogroup B, strain MC58
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.Parkhill, J.; Adgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A.Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daseplate assembly protein V, probable NMB1111 [imported] - Neisseria meningitidis (stra Cispecies: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: D81122; A81901
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; It, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Fizza, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84572.1; PID:g7379996
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C<u>. Ac</u>ces<u>sio</u>n: D72252
R;Nelsón, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ve
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B9667
A;Status: prealiminary
A;Molecule type: DNA
A;Residues: 1-476 <STO>
A;Cross-references: GB:AE005173; NID:g10645403; PIDN:AAG21521.1; GSPDB:GN00141
A;Genetics:
A;Genetics:
A;Genetics: A;Anp position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755
A;Accession: D81122
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C;Date: 11-Jun_1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 476;
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37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.5;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 KLSKLEKKLAEEGTEKLKLAK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLAKLAKKLA-----KLAK 14
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
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LSKLAKKTAQTAK 15
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Matches 9; Conserv
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Matches 12; Conserv
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A;Molecule type: DNA
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C;Accession: $45598; $43556
R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Eur. J. Blochem. 222, 267-276, 1994
A;Title: Streptokinase activates plasminogen bound to human group C and G streptococc A;Reference number: $45598; WUID:94291620
A;Accession: $45598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: D81284
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 403, 665-668 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-455 <PAR>
A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73819.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptococcus sp.
C;Date: 14-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA A;Residues: 1-454 <BE2>
A;Residues: 1-454 <BE2>
A;Cross-references: EMBL:Z32677; NID:g474767; PIDN:CAA83588.1; PID:g474768
C;Superfamily: M5 protein
A; Wolecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Cross-references: EMBL:X58179; NID:947364; PIDN:CAA41168.1; PID:947365 C; Genetics: A; Gene: emm C; Genetics: emm C; Superfamily: M5 protein C; Keywords: transmembrane protein C; Keywords: transmembrane protein F; 1-417-0main: signal sequence #status predicted <SIG> F; 42-436/Product: M protein #status predicted <MMT> F; 1-427-0main: transmembrane #status predicted <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasminogen-binding protein MLC36 - Streptococcus sp. (fragment)
                                                                                                                                                                                                                                                                                                                                                             Length 436;
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Pred. No. 99;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2
Pred. No. 96;
2; Mismatches
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C,Superfamily: fumarate hydratase
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 75.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 KLAKQAEELAKL 355
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Best Local Similarity
Matches 9; Conserv
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Mol. Gen. Genet. 237, 287-300, 1993

A;Ittle: Three different types of organization of the vir regulon in group A streptococd A;Reference number: $30283; MUID:93204905

A;Reference number: $30284

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-436 <PODI>
A;Residues: 1-436 <PODI>
A;Cross-references: EMBL:X58179

B;Podbielski, A: Melzer, B.
B;Podbielski, A: Melzer, B.
B;Podbielski, A: Melzer, B.
B;Podbielski och the EMBL Data Library, February 1991

A;Description: Por mediated cloning and sequencing of group A streptococcal emm41/52 (ev A;Reference number: $29680

A;Recession: $29681
                                                                                                                                                                                                                                                                                                                                                                                   cmk protein precursor - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: D64830; 141019; 549998
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D64830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: GB:AE000193; GB:U00096; NID:91787134; PIDN:AAC73995.1; PID:91787138; A.Cross-references: Strain K-12, substrain MG1655
R.Experimental Source: strain K-12, substrain MG1655
R.Fricke, J.; Neuhard, J.; Kelln, R.A.; Pedersen, S.
J. Bacteriol. 177, 517-523, 1995
J. Bacteriol. 177, 517-523, 1995
A.Fille: The cmk gene encoding cytidine monophosphate kinase is located in the rpsA open A.Reference number: 141019; MUID:95138007
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C;Species: Streptococcus pyogenes
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: S30284; S29681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA A;SESLEMSSV, 251, 'SPL' <RES> A;Residues: 158-248, 'DVRNTSVIVSPLVSKSLSSLRWSSV', 251, 'SPL' <RES> A;Cross-references: EMBL:X82933; NID:9599733; PIDN:CAA58106.1; PID:9599734 A;Experimental source: strain K-12; plasmid pSP547
                                                                                                                      Gaps
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                                                              Length 262;
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                                                              DB 2;
                                                        Score 39; DB 2
Pred. No. 61;
3; Mismatches
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                                                        62.9%;
ilarity 57.1%;
Conservative
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77 KSSKYGKRLAKIAK 90
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77 KSSKYGKRLAKIAK 90
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les 8; Conser
                                                                                       Best Local Similarity
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                                                              Query Match
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N: Alternate names: forty protein

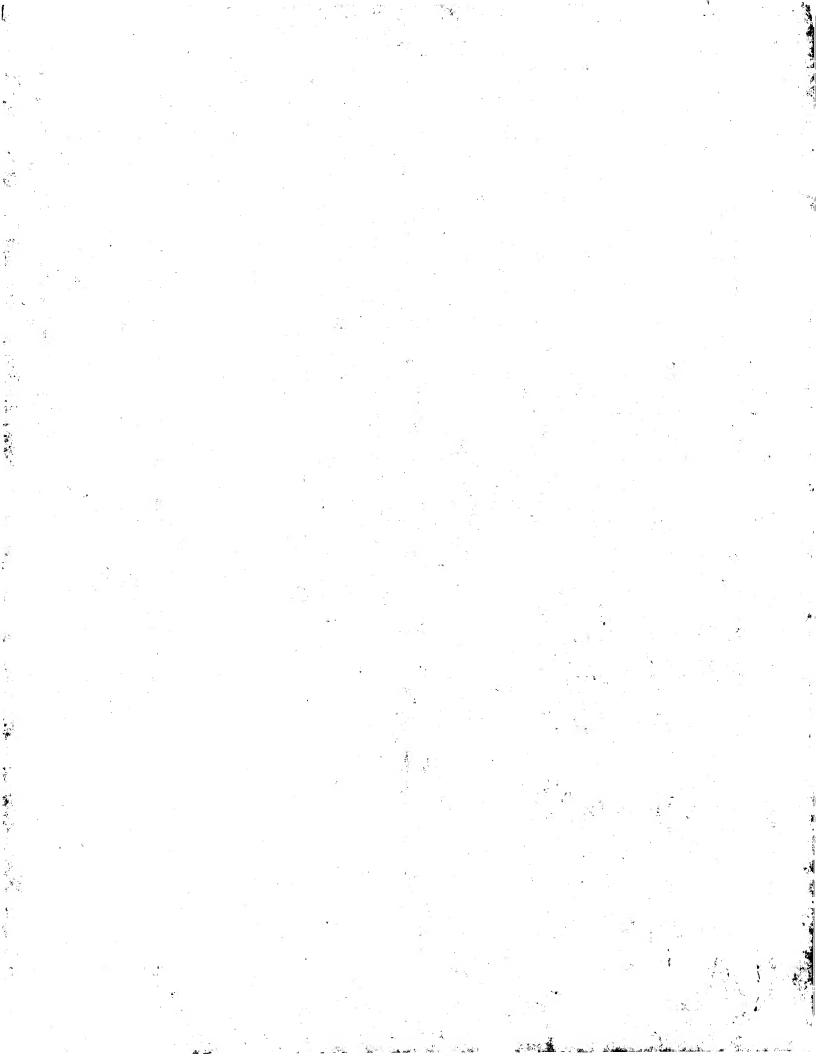
C; Species: Streptococcus sp.
C; Date: 30.Sep-1993 #text_change 26-Aug-1999
C; Accession: JG1419; S17354
R; Smirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Zav'yalov, V.P.
G; Snirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Zav'yalov, V.P.
G; Snirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Sav'yalov, V.P.
G; Snirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Sav'yalov, V.P.
G; Snirnov, O.Y.; Denesyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Sav'yalov, V.P.
G; Reference number: JG1419; MJD:93013016
A; Reference number: JG1419; MJD:93013016
A; Reference number: JG1419; MJD:93013016
A; Reference number: JG1419
A; Residues: J-587 cSMI>
C; Genetics:

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                 A. Cross references (1998). NID: 9153616; PIDN: AAA26874.1; PID: 9153617
R: Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
Mol. Microbiol. 14, 619-631, 1994
A. Title: Non-congruent relationships between variation in emm gene sequences and the A; Reference number: $60802
A; Recession: $60802
A; Recession: $60802
A; Mull: Speliminary; nucleic acid sequence not shown; not compared with conceptual A; Molecule type: DNA
A; Recides: 30-89 < WHM>
C; Superfamily: M5 protein
C; Keywords: coiled coil; transmembrane protein
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
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JC1419
Fc gamma (IgG) receptor II precursor - Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; 1
Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.9%;
75.0%;
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Matches 9; Conservative
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447 KLAKQAEELAKL 458
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A; Residues: 1-539 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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A; Variety: serotype M24
A; Variety: serotype M24
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 26-Aug-1999
C; Accession: A28849; S60802
R; Mouw, A.R.; Beachey, E.H.; Burdett, V.
J. Bacteriol. 170, 676-684, 1988
A; Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence A; Reference number: A28549; MUID:88115166
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                      C; Species: Streptococcus sp.
A; Variety: group G
C; Date: 07-Sep-1994; #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C; Accession: 845599; 843554
R; ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebring, U.
Biochem. 222, 267-276, 1994
A; Title: Streptokinase activates plasminogen bound to human group C and G streptococci A; Reference number: S45598; MUID:94291620
A; Accession: S45599
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A;Status: preliminary
A;Status: 1-472 - 26E2>
A;Residues: 1-472 - 26E2>
A;Cross-references: EMBL:Z32678; NID:g474769; PIDN:CAA83589.1; PID:g1333838
C;Superfamily: M5 protein
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A;Residues: 1-532 vepD>
A;Cross-references: EMBL:X60097; NID:g840905; PIDN:CAA42693.1; PID:g840906
C;Superfamily: M5 protein
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                                                                                                                                                                                                                                                                         plasminogen-binding protein MLG72 - Streptococcus sp. (fragment)
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Pred. No. 1.1e+02;
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Pred. No. 1e+02;
2; Mismatches
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A28549
M24 protein precursor - Streptococcus pyogenes
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75.0%;
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75.0%;
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Best Local Similarity 75.uv,
Procal 9; Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                :| :|| ||||||
131 ELKAIAKALAKLAK 144
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440 KLAKQAEELAKL 451
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S54871
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A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630
A; Recession: C64071
A; Accession: C64071
A; Recession: C64071
A; Recession: C64071
A; Residues: 10-142 carGRA
A; Residues: 1-142 carGRA
A; Residues: 1-142 carGRA
A; Cross-references: GB:U32730; GB:L42023; NID:93312191; PIDN:AAC22136.1; PID:91573456; T
C; Superfamily: H+-transporting ATP synthase epsilon chain
C; Reywords: ATP biosynthesis; hydrolase; membrane-associated complex
Query Match
Best Local Similarity 72.7%; Pred. No. 50;
Matches B; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
A 2 LAKLAKKLAKL 12
Db 118 VAKLSKELAKL 128
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Search completed: May 8, 2002, 07:19:31 Job time: 99 sec



chimera_x.rspt

burkholderi burkholderi P70944 burkholderi

09m214 arabidopsis 091128 pseudomonas 091420 erwinia amy 09tyq0 drosophila 09pcz4 xylella fas 013375 saccharomyc 09ev42 alcaligenes 09c524 arabidopsis P75810 escherichia 065877 barley yell 065877 barley yell

092521 barley yell 09uwe0 aspergillus 09vzh4 drosophila 09rj38 streptomyce 076414 caenorhabdi

Q9jla7 barley yell Q9izg0 barley yell Q9hw35 pseudomonas Q9w3w9 drosophila Q9a386 caulobacter Q9pkq7 chlamydla m

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Rothstein S.J., Jorgensen R.A., Yin J.C.P., Yong-Di Z., Johnson R.C., Reznikoff W.S.; "Genetic organization of Tn5."; "Genetic organization of Tn5."; Cold Spring Harb. Symp. Quant. Biol. 45:99-105(1981).
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MEDLINE=83050973; PubMed=6291786;
Johnson R.C., Yin J.C.P., Reznikoff W.S.;
Control of Tn5 transposition in Escherichia coli is mediated by protein from the right repeat.";
Cell 30:873-882(1982).
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Escherichia.
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SEQUENCE OF 382-395 FROM N.A.
MEDILNE-83106478; Pubmed-6295884;
MEDILNE-83106478; Q., Auerswald E.A., Reiss B., Schaller H.;
Beck E., Ludwig G., Auerswald E.A., Reiss B., Schaller H.;
"Nucleotide sequence and exact localization of the neomycin phosphotransferase gene from transposon Tn5.";
Gene 19:327-336(1982).
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MEDLINE-82049482; PubMed-6271452;
Auerswald E.A., Ludwig G., Schaller H.;
"Structural analysis of Th5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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MEDLINE-81162719; PubMed-6260374;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Rothstein S.J., Reznikoff W.S.;
"The functional differences in the inverted repeats of Tn5 are caused
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MEDLINE-82049532; Pubmed-6271497;
Rothstein S.J., Jorgensen R.A., Yin J.C.P., Yong-Di Z., Johnson R.C.,
Reznikoff W.S.;
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MEDLINE-83050973; PubMed-6291786;
Johnson R.C., Yin J.C.P., Reznikoff W.S.;
"Control of Tn5 transposition in Escherichia coli is mediated protein from the right repeat.";
Cell 30:873-882(1982).
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                                                                             SEQUENCE FROM N.A.
MEDILINE-81345055;
MEDILINE-81345055;
Johnson R.C., Reznikoff W.S.;
"DNA sequences at the ends of transposon In5 required for transposition.";
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InterPro; IPR003201; Transposase_Tn5.
Pfam; PF02281; Transposase_Tn5; 1.
SEQUENCE 395 AA; 44757 MW; CBE32E0F62E84B8C CRC64;
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"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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Cold Spring Harb. Symp. Quant. Biol. 45:99-105(1981)
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Rothstein S.J., Reznikoff W.S., \mbox{\tt "The functional differences in the inverted repeats of Tn5 are caused <math display="inline">\mbox{\tt "The functional differences}
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Johnson R.C., Yin J.C.P., Reznikoff W.S.;
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Cell 30:873-882(1982).
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Berg D.E.;
(In) Berg D., Howe M. (eds.);
Mobile DNA, pp.163-184, American Scoiety for Microbiology, Washington DC (1989).

EMBL; U00004; AAA73394.1; -.
Johnson R.C., Reznikoff W.S.; "DNA sequences at the ends of transposon Tn5 required for
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Pfam; PF02281; Transposase_Tn5; 1.
SEQUENCE 421 AA; 47572 MW; D6C54358246F5D56 CRC64;
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MEDLINE-22049482; PubMed=6271452;
Auerswald E.A., Ludwig G., Schaller H.;
"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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SEQUENCE FROM N.A.
MEDLINE=81162719; Pubmed=6260374;
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SEQUENCE FROM N.A.
MEDLINE-81162719; PubMed=6260374;
Rothstein S.J., Reznikoff W.S.;
"The functional differences in the inverted repeats of Tn5 are caused by a single base pair nonhomology.";
Cell 23:191-199(1981).
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MEDLINE-82049532; Pubmed=6271497;
Rothstein S.J., Jorgensen R.A., Yln J.C.P., Yong-Di Z., Johnson R.C.,
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MEDLINE=83050973; PubMed=6291786;
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Mobile DNC, pp.163-184, American Scoiety for Microbiology,
Washington DC (1989).
EMBL; U00004; AAA73393.1; -.
EMBL; V00617; CAA23891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson R.C., Reznikoff W.S.; "DNA sequences at the ends of transposon Tn5 required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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SEQUENCE 476 AA; 53304 MW; 737FA045F13D3D42 CRC64;
                                                                                                                                                                                                                                                             Auerswald E.A., Ludwig G., Schaller H.,
"Structural analysis of Tn5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
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                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                       476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%; Score 49;
31.8%; Pred. No.
Live 15; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR003201; Transposase_Tn5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-83245055; Pubmed-6306482;
                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-82049482; PubMed-6271452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genetic organization of Tn5.";
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Best Local Similarity 31.8%
Matches 7; Conservative
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                                       PRELIMINARY;
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                                                                                                                                             Escherichia coli
                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                         PROTEIN #1.
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Q46731;
                                     Q57460
Q57460;
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Q46731
ID Q46
AC Q46
DT 01:
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Q57460
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Escherichia.
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(In) Berg D., Howe M. (eds.);
Mobile DNA, pp.163-184, American Scoiety for Microbiology,
Washington DC (1989).
EMBL; U00004; AAA73388.1; -.
EMBL; V00615; CAA23888.1; -.
InterPro: IPR003201; Transposase_Tn5.
Pfam; PF02221; Transposase_Tn5.
Pfam; PF02221; Transposase_Tn5.
SEQUENCE 450 AA: 50488 MW; C655574EA917AAC3 CRC64;
SEQUENCE FROM N.A.
MEDLINE-83245055; PubMed-6306482;
Johnson R.C., Reznikoff W.S.;
"DNA sequences at the ends of transposon In5 required for
                                                                                                                                                                                                                                                                                                                                 Length 450;
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4 64 1 -> Y (IN REF. 2).

5 200 K -> R (IN REF. 2).

5 225 Y -> I (IN REF. 2).

3 33 8 -> G (IN REF. 2).

AA; 50490 MW; 49BDEDDA6628C89F CRC64;
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Structural analysis of Th5.";
Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).
EMBL. 915572; AAB60063.1;
InterPro; IPPR003201; Transposase_Tn5.
Pfam; PF02281; Transposase_Tn5.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSPOSON TN5 IS50L.
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31.8%; Pred. No. 89;
iive 15; Mismatches
                                                                                                                                                                                                                                                                                                                               87.5%; Score 49; DB 2; 31.8%; Pred. No. 89;
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"The revised nucleotide sequence of Tn5.";
Gene 154:129-130(1995).
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MEDLINE=95172393; PubMed=7867940;
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Best Local Similarity 31.8%
Matches 7; Conservative
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                                                                   transposition.";
Nature 304:280-282(1983).
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SEQUENCE FROM N.A.
TRANSPOSON=TN5;
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Matches 7; Conserv
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CONFLICT
SEQUENCE
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Q46730 Q46730;

RESULT 046730

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Gaps

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Query Match

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CONFLICT CONFLICT

SO DE LA SECTION DE LA SECTION

Gaps

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Indels

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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham.X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham.X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnegle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                           Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.9%; Score 47; DB 2; Length 398; 30.4%; Pred. No. 1.7e+02; ive 15; Mismatches 1; Indels
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InterPro; IPR00160; DUF9.
Pfam; PF00990; DUF9; 1.
SMART; SM00267; DUF1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 398 AA; 44408 MW; 2A9C33E6AFA7CC79 CRC64;
                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN PA1107.
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Last annotation update)
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                           DB 2;
95;
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                                                         Mismatches
                            87.5%; Score 49;
31.8%; Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                         15;
                                                                                    2 MSIARLGGXXXXXXXXXXX 23
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Best Local Similarity 30.4*
"-has 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen.";
Nature 406:959-964(2000).
                                                         Conservative
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                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                            Query Match
Best Local Similarity
Matches 7; Conserv
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CG2996.
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                                                                                                                                                                                                                                                                                                                       Pseudomonas
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                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"Structural analysis of Tn5.";

Cold Spring Harb. Symp. Quant. Biol. 45:107-113(1981).

EMBL, U15573, AAB66064.1; -.

InterPro: IPR003201; Transposase_Tn5.

Ffam: PF02281; Transposase_Tn5.

CONFLICT 200 200 K -> R (IN REF. 2).

CONFLICT 225 225 Y -> I (IN REF. 2).

CONFLICT 325 225 Y -> I (IN REF. 2).

CONFLICT 333 303 S -> G (IN REF. 2).

SEQUENCE 476 AA; 53306 NW; B52F2F143646AF10 CRC64;
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Cai Y., Wolk C.P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 88:5355-5359(1991)
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"The revised nucleotide sequence of Tn5.";
Gene 154:129-130(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
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                                                                                                                                TRANSPOSON-TN5;
MEDLINE-95172393; PubMed-7867940;
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MEDLINE=82049482; PubMed=6271452;
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31.8%; Pre
tive 15;
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Best Local Similarity 31.00
Best Local Similarity 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified bacterium
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Wolk C.P.;
                                                                        Escherichia.
NCBI_TaxID=562;
                           TRANSPOSASE.
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SEQUENCE 1
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Q57047;
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Q57047
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Gaps

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RESULT
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Matches

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Winstanley C., Hales B.A., Corkill J.E., Gallagher M.J., Hart C.A.; "Flagellin gene variation between clinical and environmental isolates of Burkholderia pseudomallei contrasts with the invariance among clinical isolates.";
                                                                                                                                                                                       FLAGELLIN (FRAGMENT).
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                     249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Med. Microbiol. 47:689-694(1998).
EMBL; AF030241; AAC27443.1; -.
InterPro; IPR001029; Flagellin_C.
ProDom; PD000316; Flagellin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
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J. Med. Microbiol. 47:689-694(1998).
EMBL. AF030240; AAC27442.1;
InterPro: IPR001029; Flagellin_C.
ProDom; PD000316; Flagellin_C: 1.
                     PRT;
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MEDLINE=99093016; PubMed=9877189;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=E956;
MEDLINE=99093016; PubMed=9877189;
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Best Local Similarity 26.1.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28450;
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                                                                                                                                                                                                                                                                                              Burkholderia
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SEQUENCE
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SEQUENCE
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                     084994
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                        ID DOT DOT SELECT REPORTS OF S
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rodorge R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,
R. Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Handon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Handon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Ballew R.M., Basu A. Baxendale J., Baytaktarolu L., Beasley E.M.,
R. Beeson K.Y., Basu A. Baxendale J., Baytaktarolu L., Beasley E.M.,
R. Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M. Dougen M. Broks B.D., Dour L. B.,
R. Borkova D., Botchan A.C., Forraz C., Forraz C., Forraz C., Forraz C., Brantis M.L.,
R. Harris M.L., Harvey D., Heilman T.J., Herrandez J.R., Hotchum K.A.,
R. Hostin D., Houston K.A., Harvey D., Heilman T.J., Herrandez J.R., Hotchum K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Malushina N.V., Li J.J., Li Z., Liang Y., Lia Z.,
Alazon D.M., Pittman G.S., Ponlard J., Wobhrefi A.,
Rethiov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Rethert K., Remington K., Saunders R.D., Verly V., Pare B.,
Spier E., Spradling A.C., Stapleton M., Stuong R., Santh H.,
Spier E., Spradling A.C., Stapleton M., Stuong R., Sant M.,
Spier E., Spradling A.C., Stapleton M., Stuong S., Yao Q.A.,
Wang Z.-Y., Wassarman D.A., Woller E., Wan D., Santh H.,
Spier E., Spradling A.C., Stapleton M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 3.
Calcium-binding; EGF_1ike domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 4215 AA; 470517 MW; 53613E810BA8D4F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro: IPR002123; Acyltransferase. Interpro: IPR000152; Asx_hydroxyl. Interpro: IPR0000859; CuB., Interpro: IPR0000861; CuB., Interpro: IPR0000861; EGF-hand. Interpro: IPR000742; EGF_2. Interpro: IPR0001881; EGF_2. Fam. PF01553; Acyltransferase; 1. Pfam; PF01553; Acyltransferase; 1. Pfam; PF00008; EGF; 6.
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SMART; SM00179; EGF_CA; 2.
SMART; SM00011; EGF_LIKe; 6.
PROSITE; PS00010; ASX_HVDROXYL; 2.
PROSITE; PS01180; CUB; 29.
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Best Local Similarity
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                         FLAGELLIN (FRAGMENT).
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria: Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 254 AA; 25363 MW; 7EEE33271B33BA71 CRC64;
                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
254 AA.
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RESULT 12 09WWT2

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RA TUNGPICE FROM N.A.

RA TUNGPARABALI S., Wajanarogana S., Tunpiboonsak S., Panyim S.;

RA TUNGPARABALI S., Wajanarogana S., Tunpiboonsak S., Panyim S.;

RA TUNGPARAGALION ondonuclease of the flagellin sequences for indentification of Burkholderia pseudomallei and Burkholderia cepacia RT from clinical isolates.";

RL MOI. Cell. Probes 0:0-0(1999).

REMBL, AF080250; AAD12054.1;

DR EMBL, AF080259; AAD12053.1;

DR InterPro: IPR001492; Flagellin_C.

DR InterPro: IPR001492; Flagellin_N.

DR Pfam; PF00669; Flagellin_N.

DR Pfam; PF00700; Flagellin_C; 1.

DR Pfam; PF00700; Flagellin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brett P.J., Woods D.E.;
"Vaccine Strategies for Immunoprophylaxis Against Melioidosis.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081500; AAC31986.1; -
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
                                                                                                                                                                                                                                                                                                                                                                                            Burkholderia thailandensis.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
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Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%; Score 46; DB 2; Length 383; 26.1%; Pred. No. 2.5e+02; tive 16; Mismatches 1; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                              383 AA.
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                                                                                                                                                                                                 PRT;
                                163 SMSAAKIGGGLVQTGQTLGTFKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SMSIARLGGXXXXXXXXXXX 23
1 SMSIARLGGXXXXXXXXXXXX 23
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                                                                                                                                                                                                 PRELIMINARY;
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Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=E264;
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NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                          FLAGELLIN.
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                                                                                                                                                                                           086045
086045;
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                                                                                                                                   RESULT 14
086045
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Q9Z3A8
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A Majanarogana S., Tungpradabkul S., Panyim S.;

T "Variation of fiagellin genes between virulent and non-virulent

T strains of Burkholderia pseudomallei.";

Submitted (JUL-1998) to the EMBL/Genbank/DDBJ databases.

EMBL; AF078153; AAD24678.1;

R InterPro; IPR001029; Flagellin_C.

R InterPro; IPR001492; Flagellin_N.

Pfam; PF00669; Flagellin_N; 1.

Pfam; PF00700; Flagellin_C; 1.

PRINTS; PR001207; Flagellin_C; 1.

PRINTS; PR001207; Flagellin_C; 1.

PRINTS; PR00016; Flagellin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=E 276;
Wajanzogana S., Tungpradabkul S., Panyim S.;
Wajanzogana S., Tungpradabkul S., Panyim S.;
Wariation of flagellin genes between virulent and non-virulent
strains of Burkholderia pseudomallel.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078155; AAD24680.1;
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
Pfam; PF00669; Flagellin_N:
Pfam; PF006700; Flagellin_C; 1.
                                                                                                                                                                                                                  Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria: Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095660;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FLAGELLIN (FRAGMENT).
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                                                 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRO0207; FLAGELLIN.
Probom: PD000316; Flagellin_C; 1.
NON_ITS 3820110 C; 1.
SEQUENCE 382 AA: 38690 MW; 68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 SMSAAKIGGGLVQTGQTLGTFKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 26.1%
Matches 6; Conservative
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Matches 6; Conservative
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                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28450;
                                                                                                                                                                                                                                                                                   Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                 Q9WWT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           098640
                                                                                 O9WWT2
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Q9S640
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Gaps

SQ SEQUENCE 383 AA; 38657 MW; 1B53B946EA01070E CRC64;

0; Gaps Query Match

82.1%; Score 46; DB 2; Length 383;
Best Local Similarity 26.1%; Pred. No. 2.5e+02;
Matches 6; Conservative 16; Mismatches 1; Indels

; 0

Search completed: May 8, 2002, 07:29:58 Job time: 111 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 07:28:07; Search time 12.9 Seconds (without alignments) 65.371 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Length	88	ID	Description
1	46	82.1	498	Н	ام	Q03413 xenopus lae
7	45	80.4	305	7	SCRK_ECOLI	3 escheric
3	45	80.4	450	П	V50K_BYDVP	P09516 barley yell
4	45	80.4	886	П	DSC1_MOUSE	
S	45	80.4	1895	Н	YLK3_CAEEL	P41951 caenorhabdi
9	44		197	П	PAAD_AERPE	Q9ybf0 aeropyrum p
7	44	œ.	221	Н	YM14_ARCFU	-
80	44	œ.	307	П	SCRK_KLEPN	
6	44	78.6	307	Н	SCRK_SALTY	P26984 salmonella
10	44	œ.	320	П	YDJE_BACSU	034768 bacillus su
11	44	ω.	496	-	IMDH_METJA	
12	44	æ	700	Н	RIR1_BACSU	P50620 bacillus su
13	44		196		YS8A_CAEEL	Q09625 caenorhabdi
14	44	œ.	1315		CHAO_DROME	_
15	43	ė.	162		COAD_XYLFA	
16	43		214		YPU5_RHOCA	
17	43	ė	236		RPC1_LAMBD	_
18	43	ė.	270		DHMA_FLAS1	
19	43	ė	282		MIND_CHLVU	
20	43	ė	286		MIND_MESVI	Q9mum5 mesostigma
21	43		351		PERX_SOLTU	P12437 solanum tub
22	43	ė.	364		PER1_LYCES	
23	43	9	386		YD46_MYCTU	_
24	43	ė.	392		YL78_ARCFU	
25	43	ė.	399		EFTU_SYNY3	
26	43	ė.	430		CLPX_BORBU	
27	43	ė.	459		HN3B_MOUSE	
28	43	ė.	469		EXOC_AZOBR	
29	43	ė.	481		IMDH_HELPJ	
30	43	ė.	481		IMDH_HELPY	P56088 helicobacte
31	43	76.8	509		5HT_LYMST	Q25414 lymnaea sta
32	43	ė.	265		UBPN_HUMAN	Q9uk80 homo sapien
33	43	9	995		UBPN_MOUSE	Q9qz16 mus musculu

011024 mycobacteri P04264 homo sapien	4 10 01 10 10	P77790 escherichia P54702 salmonella P10718 rhodospiril P50653 acetobacter Q02437 hordeum vul	
YD54_MYCTU K2C1_HUMAN	VIBA_RAIME VIB4_AGRT9 AAP1_YEAST AHM6_ARATH YTR6_AZOBR	DDPX_ECOLI FLIR_SALTY RCEM_RHORU QOX2_ACEAC E13D_HORVU	ALIGNMENTS
623 1 643 1	7489 1856 1949 1949	193 1 264 1 305 1 307 1 327 1	
76.8	76.8 76.8 76.8 75.0	75.0 75.0 75.0 75.0	
444	4 4 4 4 0 6 6 6 6	4444	
9.84 4.73	33 33 40 40	4 4 4 4, 1 2 6 4 4 5	

AA.	e) ite) OG (SERUM RESPONSE FACTOR-	MEF2D OR SL1. Xenopus laevis (African clawed frog). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. NCBI_TaxID=8355;	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-93099873; PubMed-1281451; Chambers A.E., Kotecha S., Towers N., Mohun T.J.; "Muscle-specific expression of SRF-related genes in the early embryo of Kenopus laevis."; EMBO J. 11:4981-4991(1992).	FUNCTION: MAY REGULATE MUSCLE-SPECIFIC TRANSCRIPTION IN THE BENERYO AND MAY REGULATE TRANSCRIPTION OF A VARIETY OF CELL TYPES IN THE ADULT: IT BINDS TO THE SEQUENCE CTA(T/A)44AR. SUBGUNIT: BINDS DNA AS A MULTIMER, PROBABLY AS A DIMER. SUBCLIULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: RESTRICTED TO THE SOMITIC MESODERM OF EARLY EMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE TADPOLE. EXPRESSED IN ALL TISSUES EXAMINED IN THE ADULT. SEXPRESSED IN ALL TISSUES EXAMINED IN THE LATE GASTRULA. SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS. MEF2 SUBFAMILY.	ced through a collab- and the EMBL outst re no restrictions ts content is in age by and for com n://www.isb-sib.ch/an	1. 1. lear protein; DNA-binding; Activator; MADS. NARZ-TYPE (POTENTIAL).
498	update n upda HOMOLA	ta; Ve achia	, Mohr	PECIFIC IPTION EQUENCI R, PROI TO THE (MYOTON BEGIN DOMAII	ht. It is produbling a bioinformatics itute. There is as long as it camoved. Us ement (See https://examore.com/removed.	otein PE (P
PRT;	Created) Last sequence update) Last annotation update) (CER FACTOR 2D HOMOLOG (lawed frog) ata; Crania a; Mesobatr	1281451; Towers N., on of SRF-re]	TE THE SEA MUSCLE-SP TO THE SE A MULTIMER NOCLER. OY MUSCLE (DY MUSCLE (DY MUSCLE (THE MADS)	copyright. copyright. cof Bioi ss Institut tutions as nt is not r se agreemen se(isb-sib.	box. IN. K_1; 1. K_2; 1. Nuclear pr MADS. MADS. ARG/LYS
STANDARD;	OLINOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update MYOCYTE-SPECIFIC ENHANCER FACTOR 2D HOMOLOG LIKE PROTEIN 1) (SL-1).	is (African c. stazoa; Chordi rrachia; Anura Xenopus.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Neurula; MEDLINE=93099873; PubMed=1281451; Chambers A.E., Kotecha S., Towers Muscle-specific expression of SR of Xenopus laevis."; EMBO J. 11:4981-4991(1992).	FUNCTION: MAY REGULATE MUSCLE-SPECTET TRANSCRIEDRYON: MAY REGULATE TRANSCRIPTION OF A VARIENBRY AND MAY REGULATE TRANSCRIPTION OF A VARIENBRY THE ADULT. IT BINDS TO THE SEQUENCE CTA(T/A) SUBGUIT: BINDS DNA AS A MULTIMER, PROBABLY AS A SUBCELLULAR LOCATION: NUCLEAR STREET TO THE SOMITIC MEMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE EXPRESCRED IN ALL TISSUES EXAMINED IN THE ADULT. STREELOWERLOPMENTAL STAGE: EXPRESSION BEGINS IN THE LISTENDER STREET SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF FACTORS. MEFZ SUBFAMILY:	S-PROT entry is copy the Swiss Institute ean Bioinformatics I non-profit institut and this statement i requires a license a	EMBL; Z19124; CAA79531.1; HASP; P11831; 1SRS. InterPro; IPR002100; MADS-box. Pfam; PF00319; SRF-TF; 1. PRINTS; PR004042; MADSDOMAIN. PROSITE; PS00350; MADS_BOX.1; 1. PROSITE; PS00366; MADS_BOX.1; 1. PROSITE; PS0066; MADS_BOX.2; 1. Transcription regulation; Nuclear Multigene family. Multigene family. S7 MADS. DOMAIN 58 86 MEE?2 DOMAIN 3 31 ARGYL
RESULT 1 MEFD_XENLA ID MEFD_XENLA AC 003413:	01-NOV-1997 (Rel. 35, C 01-NOV-1997 (Rel. 35, L 15-DEC-1998 (Rel. 37, L MYOCYTE-SPECIFIC ENHANC LIKE PROTEIN 1) (SL-1).	MEF2D OR SL1. Xenopus laevis (Afri- Eukaryota, Metazos, Amphibia, Batrachia, Amphibia, Batrachia, Xenopodinae, Xenopus NCBI_TaxID=8355,	EQUENCE FROM N.A. TISSUE-Neurula; MEDLINE-93099873; Chambers A.E., Kot "Muscle-specific e of Kanopus laevis. EMBO J. 11:4981-49	FUNCTION: EMBRYO AN IN THE AD IN THE	This SWISS-PR between the the European use by non- modified and entities requ	EMBL, Z19124; CAA79531. HSSP; P11831; 1SRS. InterPro; IPR002100; MP Fam; PF00319; SRE-TF; PRINTS; PR00404; MADSD SMART; SMO0432; MADS; PROSITE; PS50066; MADS, PROMAIN 3 3 3 57 DOMAIN 3 3 3 100 MAIN 3 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
RESULT MEFD_X ID M	05 04 05 05 05 05 05 05 05 05 05 05 05 05 05	800008 800008	RN RC RX RT RT	88888888888	388888888	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                        DSC1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                 P55849
                                                                                                                                                                                                                                                                                                                                                     RESULT 4
DSC1_MOUSE
                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulres a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
50 RAD PROTEIN
BAILPY Pellow dwarf virus (isolate PAV) (BYDV).
Viruses; ssrNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                          Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                        Length 498;
                                                            Indels
        9E98D13D80AAF510 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AA; 33081 MW; 5F9C8D59B66C3E55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                        DB 1;
                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
FRUCTOKINASE (EC 2.7.1.4).
                                                                                                                                                      305 AA.
                                                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                       82.1%; Score 46;
ilarity 27.3%; Pred. No. 6
Conservative 15; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.4%; Score 45; 26.1%; Pred. No.
 GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                              292 MSVQRLGGVSQATHSLTTPVVS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SMSIARLGGXXXXXXXXXXX 23
                                                                               2 MSIARLGGXXXXXXXXXXX 23
         54071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 AVGIARLGGTSGFIGRVGDDPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X81461; CAA57218.1; -. InterPro; IPR002173; PfkB.
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                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fransferase; Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
366
498 AA;
                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_FTaxID=12040;
                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                6-PHOSPHATE.
                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                       STRAIN-EC3132;
                                                                                                                                                                                                                                                                                                  Bockmann J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
9
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P09516;
                                                                                                                                                     SCRK_ECOLI
P40713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luteovirus
         SEQUENCE
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 DOMAIN
                                                                                                                                           SCRK_ECOLI
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                                                                                                                                 RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-! INVEST. DETMACTO. 107:531-538(1996).

-! FUNCTION: COMPONENT OF INTERCELLUIAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ANGESION MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADMESSIVENESS BETWESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TSSUES.

-! SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.

-! ALTERNATIVE PRODUCTS: Z ISOFORMS; JA (SHOWN HERE) AND 1B; ARE PRODUCED BY ALTERNATIVE SPLICING.

-! DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         King I.A., O'Brien T.J., Buxton R.S.; "Expression of the 'skin-type' desmosomal cadherin DSC1 is closely linked to the keratinization of epithelial tissues during mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002929; PLRV_ORF5.
Pfam; PF01690; PLRV_ORF5; 1.
SEQUENCE 450 AA; 49733 MW; 5878FA9361498205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DESMOCOLLIN 1A/18 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
-!- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             886 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.4%; Score 45; 21.7%; Pred. No.
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MEDLINE=96420658; PubMed=8823356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07653; CAA30495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S00950; S00950.
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Best Local Similarity
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
modified and this statement is not removed. entities requires a license agreement (See h
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                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                      208393 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SMSIARLGGXXXXXXXXXXX 23
                                                     EMBL; U00065; AAA50735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                            461 46
569 56
1895 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAAD_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pauley A., Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
STRONG, TO 2C84.1.
-!- SIMILARITY: CONTAINS ? EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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  and for commercial
              entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
KVYLCGQAEEH -> ESIRGHTLIKN (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III
                                                                                                                                                           PROSITE; PS00232; CADHERIN_1; 2.
PROSITE; PS50268; CADHERIN_2; 4.
Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein; Calcium-binding; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 80.4%; Score 45; DB 1; Length 886; Local Similarity 26.1%; Pred. No. 1.7e+02; es 6; Conservative 15; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
 Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 1B).
F34F8D8578CE92F7 CRC64;
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1895 AA.
 and this statement is not removed.
                                                                                                                                                                                                                                                                                               CADHERIN 1.
                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                  POTENTIAL
                                                  EMBL, X97986, CAA66628.1; -.
EMBL, X97986, CAA66629.1; -.
HSSP, P09803; IEDH.
MGD; MGI:109173; DSG1.
InterPro; IPR002126; Cadherin.
Pfam; PR0028; Cadherin. 5.
PRINTS; PR002205; CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         764 SMSVGTLGGQGIKTQQSFEMVKG 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             98953 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             886 AA;
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P41951;
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DOMAIN
TRANSMEM
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CARBOHYD
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(See http://www.isb-sib.ch/announce/
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R WormPep; D1044-3; CE01206.

R InterPro; IPR000561; EGF-1ike.

R InterPro; IPR000561; EGF-1ike.

R InterPro; IPR000519; EBL.

R InterPro; IPR00059; EBL.

R InterPro; IPR00059; EBL.

R Pfam; PF00069; PKinase.

R Pfam; PF00069; WR1; 12.

R SMART; SM00289; WR1; 12.

R PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0111; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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DNA Res. 6:83-101(1999).
-!- SIMILARITY: BELONGS TO THE POLYPRENYL P-HYDROXYBENZOATE /
PHENYLACRYLIC ACID DECARBOXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.4%; Score 45; DB 1; Length 1895;
26.1%; Pred. No. 4.18+02;
Live 16; Mismatches 1; Indels
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fW; F23C9F7881353AD6 CRC64;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE AROMATIC ACID DECARBOXYLASE (EC 4.1.1.-).
APE1647.
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EMBL; AP000062; BAA80648.1; -.

SO WE DR CC

028069; YM14_ARCFU

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307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X61004; CAA43322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
                                                                                                                                                            FRUCTOKINASE (EC 2.7.1.4).
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                                                                          STANDARD;
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                                                                                                                                                                                                Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; $16037; $16037.
PIR; $18523; $18523.
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                                                                                                                                                                                                                                                 NCBI_TaxID=573;
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                                                                        SCRK_KLEPN
P26420;
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P26984;
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G. (311 S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.E., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                               Gaps
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reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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                                    n; Lyase; Decarboxylase; Complete proteome 21184 MW; BB878C6DB14C4B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.6%; Score 44; DB 1; Length 221; 28.6%; Pred. No. 55; tive 15; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                           78.6%; Score 44; DB 1; Length 197 22.7%; Pred. No. 48;
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888043795312594C CRC64;
                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN AF2214.
                                                                                                                                           17; Mismatches
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MEDLINE-98049343; PubMed-9389475;
InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Hypothetical protein; Lyase; Decark
SEQUENCE 197 AA; 21184 MW; BB87
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                                                                                                                                                                                                    163 PO
200
24925 MW;
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                                                                                                                           Best_Local Similarity 22.7%
Matches 5; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Archaeoglobus fulgidus.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                  78.6%; Score 44; DB 1; Length 307, 21.7%; Pred. No. 80;
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                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
FRUCTOKINASE (EC 2.7.1.4).
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InterPro; IPR002173; PfkB.
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                                                                                                                                                                                                                                                                           01-NOV-1997
                                                                                                                                                                                                                                                     IMDH_METJA
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                                                                                                        Query Match
                                                                                                                                                                                                                                                                 059011;
                                                                                                                                                                                                                                      IMDH_METJA
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DR
DR.
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.; "Sequence analysis of the groESL-cotA region of the Bacillus subtilis genome, containing the restriction/modification system genes."; DNA Res. 4:335-339(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                   -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
            MEDLINE-92236409; PubMed-1809835;
Aulkemeyer P., Ebner R., Hellenmann G., Jahreis K., Schmid K.,
Warieden S., Lengeler J.W.;
"Molecular analysis of two fructokinases involved in sucrose
                                                                           MO1. Microbiol. 5:2913-2922(1991).
-!- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE = ADP + D-FRUCTOSE
                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 44; DB 1; Length 307; 21.7%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last nonotation update)
HYPOTHETICAL SUGAR KINASE IN GUTA-COTA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                             ;; Kinase; Plasmid.
307 AA; 32916 MW; E01CB770CE20B329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Staphylococcus group; Bacillus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                  Pfam; PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168 / MARBURG;
MEDLINE=98116660; PubMed=9455482;
                                                                metabolism of enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 AVGVARLGGNSGFIGAVGGDPFG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB007638; BAA22760.1; -.
EMBL; 299107; CAB12436.1; -.
SubtiList; BG12796; ydjE.
                                                                                                                                                                                                                                              EMBL, X61005, CAA43323.1; -. PIR; S16044, S16044. PIR; S18524. InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                     6-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                              ransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDJE OR FRUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDJE_BACSU
034768;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDJE_BACSU
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-!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANIUE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: INOSINE 5'-PHOSPHATE + NAD(+) + H(2)O = XANTHOSINE 5'-PHOSPHATE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGENERAL FACA N. R. S. STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-9637999; PubMed=8680807;

MEDLINE-9637999; PubMed=8680807;

Bull C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Boordovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
-i- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
                                                                                                                                                                                                                                                                                                                                            ;
0
Pfam; PF00294; pfkB; 1.
PROSITE; PS00584; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
Hypothetical protein; Transferase; Kinase; Complete proteome. SEQUENCE 320 A4; 34256 MW; A54E095039953B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205) (IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                   Length 320;
                                                                                                                                                                                                                                                               DB 1;
83;
                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                   78.6%; Score 44; 26.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000644; CBS.
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR01093; IMP_DH_GMP_RED.
Pfam; PF00571; CBS; 2.
Pfam; PF00478; IMPDH_C; 1.
Pfam; PF01574; IMPDH_N; 1.
                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 SAAIAKLGGDAAFSGKVGKDPFG 65
                                                                                                                                                                                                                                                                                                                                                                                                                      1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEHYDROGENASE) (IMPDH) (IMPD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35, Created)
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                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMP REDUCTASE.
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chimera_x.rsp

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Gaps

; 0

Indels

ä

17; Mismatches

Conservative

5,

78.6%; Score 44; DB 1; Length 700; 21.7%; Pred. No. 2e+02;

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Best Local Similarity
     Query Match
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CHAO_DROME
                                                                                                                                                                                                                                                    YS8A_CAEEL
                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-97124182; PubMed-8969495; Scotti C., Valbuzzi A., Perego M., Galizzi A., Albertini A.M.; Tree Bacillus subtilis genes for ribonucleotide reductase are similar to the genes for the second class I NrdE/NrdF enzymes of Enterobacteriaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MICTOBIOLOGY 142:2995-3004(1996).

-I- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY FOR DNA SYNTHESIS (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE DIPHOSPHATE + OXIDIZED THIOREDOXIN + H(2)0 = RIBONUCLEOSIDE DIPHOSPHATE + REDUCED
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE LARGE CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDE THAN TO
                     PROSITE; PS00487; IMP_DH_GMP_RED; 1.
Oxidoreductase; NAD; GMP blosynthesis; Purine blosynthesis; Repeat;
CGS domain; Complete proteome.
DOMAIN 43 95 CBS 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY. SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                                  78.6%; Score 44; DB 1; Length 496; 21.7%; Pred. No. 1.4e+02; ive 18; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D2D4B914B97BBFA6 CRC64;
                                                                                                                                                   IP (POTENTIAL).
C3E03FDDF3898396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00317; ribonucleo_red; 1.
PROSITE; PS00089; RIBORED_LARGE; 1.
Oxidoreductase; DNA replication; Complete proteome.
SEQUENCE 700 AA; 80688 MW; D2D48914B97BBFA6 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 700 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subtilist; BG11404; nrdE.
InterPro; IPR000788; Ribonucleo_red.
                                                                                                 CBS 1.
CBS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                        61 AIALARLGGLGVIHRNMSIEEQV 83
                                                                                                                                                                                                                                                                                                                                                      1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                        53316 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z68500; CAA92810.1; -. EMBL; Z99113; CAB13622.1; -.
                                                                                                                                                                                                                                                                         Best Local Similarity 21.7% Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBONUCLEOTIDE REDUCTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                         155
306
  SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                 43
103
306
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRDE OR NRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIRI_BACSU
P50620;
                                                                                                                         DOMAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                       Query Match
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between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAO_DROME STANDARD; PRT; 1315 AA.
P12024, 09VAD1;
01-0CT-1989 (Rel. 12, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2011 (Rel. 40, Last annotation propare)
20-AUG-2011 (Rel. 40, Last annotation propare)
CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN).
CHO OR CHT OR CG1744.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%; Score 44; DB 1; Length 796; 26.1%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 84.3 KDA PROTEIN ZR945.10 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilkinson-Sproat J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76DC5B03E6357A6A CRC64;
                                                                                                                                                                  796 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER/THR-RICH.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transmembrane
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 248582; CAA88469.1; -.
EMBL; 248544; CAA88446.1; JOINED.
EMBL; 248544; CAA88444.1; -.
EMBL; 248582; CAA88444.1; JOINED.
WormPep; ZK945.10; CE01732.
                           189 SMOLSKLGGGVSLNLSKLRAKGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609 SVSMPRLGGTYPASTFVGPGNYT 631
1 SMSIARLGGXXXXXXXXXXXX 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84306 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
546
752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      796 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                       YS8A_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                ZK945.10
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Adams W.D., Celniker S.E., Holt R.A., EVANS C.A., GOCAYNB J.D.,

Adams W.D., Celniker S.E., Holt R.A., EVANS C.A., GALIB R.F.,

RA GAGOGG R.A., LEWYS S.E., Richards S., Amburner M., Henderson S.N.,

Sutton G.G., Worthman J.R., Yandell N.D., Zhang O., Chen L.X.,

Baradon R.C., Rogars Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Baradon R.C., Rogars Y.-H.C., Helt G., Nelson C.R., Miklos G.L.G.,

RA Baradon R.C., Rogars Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Cawley B. Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandre P.

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandre P.

RA Burtis K.C., Brangelista C.C., Reraca C., Perraca C., Perraca S.M., Dukov B.C., Dunn P.,

Bockova D. Botchor A., Bownes M., Dugan-Rocha S., Dunkov B.C., Dunn P.

RA Bartis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Jalail M., Kalush F., Karpen G.H., Kez', Kennison J.A., Ketchum K.A.,

RA Mextulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mextulov G., Milshina N.V., Mobarry C., Morris J., Morsh M., Nelson M.,

RA Balazzoln K., Morn M., Wurphy B., Murphy L., Waray D.M., Nelson H.,

RA Balazzoln G., Alden K., Saunders R., Venter E., Shen H.,

Raider R., Spradling A.C., Stapleton M., Stupsk M., Shen B.,

Ranger R., Spradling A.C., Stapleton M., Stupsk M., Shen G.,

Ranger B., Roger C., Turner R., Wenner S., Wan S., Sun E.,

Ranger B., Spr
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"Neuronal development in the Drosophila retina: monoclonal antibodies
as molecular probes.";
Cell 36:15-26(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL MORPHOGENESIS. MEDIATES HOMOPHILIC CELLULAR ADHESION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Head;
MEDLINE-81166231; PubMed-3920657;
Zipursky S.L., Venkatesh T.R., Benzer S.;
From monoclonal antibody to gene for a neuron-specific glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: EXPRESSED IN PHOTORECEPTOR CELLS AND THEIR AXONS IN THE ADULT RETINA, THE OCELLUS AND LARVAL PHOTORECEPTOR
                                     Reinke R., Krantz D.E., Yen D., Zipursky S.L.;
"Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell morphogenesis, contains a repeat motif found in yeast and human.";
Cell 52:291-301(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 82:1855-1859(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 30-50, AND TISSUE SPECIFICITY.
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MEDLINE-84106810; Pubmed-6420071;
                     MEDLINE=88135762; PubMed=3124963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 30-50 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Membrane; Signal; Repeat; Leucine-rich repeat; Vision. SIGNAL 1 29
PHOTORECEPTOR CELL DIFFERENTIATION, PERSISTS THROUGH DEVELOPMENT
                                                               TO A
                              -!- SIMILARITY: BELONGS TO THE CHAOPTIN FAMILY.
-!- SIMILARITY: CONTAINS 38 LEUCINE-RICH REPEATS (LRR).
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE '
FRAMESHIFT IN POSITION 1123.
                                                                                                                                                                                                                                        EMBL; M19017; AAA28425.1; ALT_FRAME.
EMBL; M19008; AAA28425.1; JOINED.
EMBL; M19009; AAA28425.1; JOINED.
EMBL; M19010; AAA28425.1; JOINED.
EMBL; M19011; AAA28425.1; JOINED.
EMBL; M19012; AAA28425.1; JOINED.
EMBL; M19013; AAA28425.1; JOINED.
EMBL; M19014; AAA28425.1; JOINED.
EMBL; M19016; AAA28425.1; JOINED.
EMBL; M2003777; AAA28425.1; JOINED.
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InterPro; IPR003591; LRR_typ.
Pfam: PF00560; LRR; 29.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 4.
SMART; SM00369; LRR_TYP; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, A29944, A29944.
FIYBASS: FBGN0000313; chp.
InterPro; IPR00025; Armadillo.
InterPro; IPR001611; LRR.
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20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H I D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T D T D D T D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T
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8, 2002, 07:30:47

Search completed: May Job time: 160 sec

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               PHOSPHOPANTETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND PYROPHOSPHATE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + PANTETHEINE 4'-PHOSPHATE = DIPHOSPHATE DEPHOSPHO-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                              -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Quagito B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M. de Rosa V.E., T., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., de Souza A.D., gerenzi M.L.Z., Siqueira W.J., de Souza A.R., Varlada H.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Sago M.A., Zatz M., Meidanis J., Setubal J.C.; The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01020; LPSBIOSNTHSS.
Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 43; DB 1; Length 162; 30.0%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: COENZYME A (COA) BIOSYNTHESIS; FOURTH STEP.-i- SUBDINIT: HOWOHEXAMER (BY SIMILARITY).
-i- SUBCELLUIAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE COAD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA; 17568 MW; 519E4052D4E364FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE003936; AAF83790.1; -- InterPro; IPR001980; LPS_Diosynth. InterPro; IPR001994; Cytidylyltransf. Pfam; PP01467; Cytidylyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 IARLGGDVSGFAPAAVVAAL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 IARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 162 AA;
         δλ
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Wed May 8 07:50:31 2002

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Мау Run on:

8, 2002, 07:28:07; Search time 22.67 Seconds (without alignments) 77.283 Million cell updates/sec

CHIMERA_X 56 Title: Perfect score:

1 SMSIARLGGXXXXXXXXXXXX Sequence:

23

BLOSUM62DX Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMMANTES	
Result		Query				
No.	Score	Match	Match Length	8	O.	Description
Н	47	83.9		7	D83506	conserved hypothet
7	46	82.1		7	S28059	serum response fac
e	46	82.1		7	T47846	Arm repeat contain
4	45	80.4	283	~	C83338	hypothetical prote
Ŋ	45	80.4		-	S52161	probable fructokin
9	45	80.4	338	7	B82660	fructokinase XF161
7	45	80.4	384	7	689965	probable fructokin
80	45	80.4		-	E64822	
6	45	80.4		7	A85595	probable DEOR-type
10	45	80.4	449	7	JQ1419	hypothetical 49.8K
11	45	80.4		7	800950	hypothetical prote
12	45	80.4		7	T33240	hypothetical prote
13	45	80.4		7	F83100	Ω,
14	45	80.4		7	E81706	conserved hypothet
15	45	80.4	1895	7	T15881	hypothetical prote
16	44	78.6	131	~	C75510	hypothetical prote
17	44	78.6	197	~	C72545	o
18	44	78.6	208	~	T25975	hypothetical prote
19	44	78.6	211	7	B84035	
20	44	78.6	221	~	F69526	conserved hypothet
21	44	78.6	240	~	н69926	ribonucleoside-dip
22	44	78.6	305	~	C85878	D-fructokinase [im
23	44	78.6	307		S18523	fructokinase (EC 2
24	44	78.6	307	-	S18524	fructokinase (EC 2
25	44	78.6	320	7	A69789	fructokinase homol
26	44	78.6	391	7	F72552	hypothetical prote
27	44	78.6	431	7	S60897	serine transport p
28	44	78.6	496	-	G64501	IMP dehydrogenase
29	44	78.6	672	~	B84782	probable receptor-

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Gaps

; 0

Query Match 82.1%; Score 46; DB 2; Length 498; Best Local Similarity 27.3%; Pred. No. 1e+02; Matches 6; Conservative 15; Mismatches 1; Indels

					-
conserved hypothet ribonucleoside-dip	nypolnetical plote ribunucleotide red chaoptin precursor		hypothetical prote membrane transloca	lipopolysaccharide hypothetical prote repressor protein	hypothetical prote N-acylmannosamine cell division inhi
H83428 B69667	T21460 T12925 A29944	E85649 S76238	T48528	C82738 S17807 RPBPL	G85513 A43744 T07303
000	777	01010	100	777	240
700	1084 1134	1578	23/4 116 133	162 214 237	237 271 282
78.6	78.6 78.6 78.6	78.6	76.8 76.8	76.8 76.8 76.8	76.8 76.8 76.8
4 4 4	4 4 4 4 4 4	7 7 7	4 4 4 3 3 3	4 4 4 w w w	444
30	337 34 34	36	38 8 30 8 30 8	4 4 4 0 1 2	43 44 5

ALIGNMENTS

	RESULT 1
	consover hypothetical protein PA1107 [imported] - Pseudomonas acruginosa (strain PAO C:Species: Pseudomonas acruginosa
	C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
	R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.: Yuan, Y.: Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbiq, K.; L
	.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
	A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
	A; Accession: D83506
	A; Molecule type: DNA A: Residues: 1-398 <syo></syo>
	A; Cross-references: GB: AE004541; GB: AE004091; NID: 99947024; PIDN: AAG04496.1; GSPDB:GN
	C; Genetics: A; Gene: Pall07
	Query Match 83.9%; Score 47; DB 2; Length 398; Best Local Similarity 30.4%; Pred. No. 52; Matches 7; Conservative 15; Mismatches 1; Indels 0; Gaps 0;
-	Qy 1 SMSIARLGGXXXXXXXXXXX 23
	Db 298 SDSVARLGGEBFLLLLPDTAEQQ 320
	RESULT 2 S28059
	serum response factor-related protein SL1 - African clawed frog
	C.)Species: Aenopus idevis (Ailican clawed 1109) C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000 Clarcesion: 978059
	R;Chambers, A.E.; Kotecha, S.; Towers, N.; Mohun, T.J. FMRO.T 11. 4081-4091 1992
	A.Title: Muscle-specific expression of SRF-related genes in the early embryo of Xenop A;Reference number: \$28059; MUID:93099873
	A; Accession: \$28059 A; Molecule type: mRNA A: Doce to the control of the control
	L:219124; NID:965204; PIDN:CAA79531.1; PID sponse factor DNA-binding domain homology
	F;2-57/Domain: serum response factor DNA-binding domain homology <srf></srf>

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A; Status: preliminary
A; Molecule type: DNA
A; Residuas: 1-338 <SIN>
A; Residuas: 1-338 <SIN>
A; Residuas: 1-338 <SIN>
A; Cross-references: GB: AE003988; GB: AE003849; NID: 99106653; PIDN: AAF84419.1; GSPDB: GN
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
B; Simpson, A.J.G.; Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000.
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chdo, M.A.; Madeira, A.M.B.N.; Madelara, H.M.F.; Mariaca, E.C.; Franco, E.C.; Mayaki, C.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R.G.; Santaltos, M.Y.; Rosa, A.J., de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.; A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.; A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.; A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.; A.C.R.; da Silva, A.D.; Sava, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.; A.C.R.; da Silva, M.A.; Verice, A.D.; Silva, A.D.; Vertcor, A.D.; A.C.R.; da Silva, M.A.; Verice, C.M.; Welference number: A.D.; Verice, A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Xylella fastidosa
C; Date: 18-Aug 2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C; Accession: B8260
K; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717
A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable fructokinase F28G11.11 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96689
                                                                                                                                                             A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-305 <BOC>
A.Residues: 1-305 <BOC>
A.Cross-references: EMBL:X81461; NID:g608705; PIDN:CAA57218.1; PID:g608707
C;Superfamily: ribokinase
C;Reywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                submitted to the EMBL Data Library, September 1994 A; Reference number: S52160 A; Accession: S52161
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.4%; Score 45; DB Best Local Similarity 26.1%; Pred. No. 91; Matches 6; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AVAVARLGGAVQFVGMLGRDMFG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SMSIARLGGXXXXXXXXXXX 23
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Best Local Similarity
Matches 5; Conserv
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C; Accession: S52161
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R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, I. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Reference number: A82950; WUID:20437337
A;Accession: C83338
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                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T47846
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24478
A;Accession: T47846
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                     Arm repeat containing protein-like - Arabidopsis thaliana
NiAlternate names: protein TBB10.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A;Introns: 504/3; 531/3; 575/3; 647/3; 679/2; 700/3; 759/2; 861/3
A;Note: T8B10.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.1%; Score 46; DB 2; Length 928; 26.1%; Pred. No. 2e+02;
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A;Experimental source: cultivar Columbia; BAC clone T8B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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probable fructokinase (EC 2.7.1.4) - Escherichia coli
C:Species: Escherichia coli
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16; Mismatches
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Pred. No.
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                                                                           292 MSVQRLGGVSQATHSLTTPVVS 313
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26.1%;
                                2 MSIARLGGXXXXXXXXXXXX
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Best Local Similarity 26.1
Matches 6; Conservative
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-283 <STO>
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Rjueng, P.P.; Vincent, J.R.; Kawata, E.E.; Lei, C.H.; Lister, R.M.; Larkins, B.A. J. Gen. Virol. 73, 487-492, 1992
A;Title: Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV isolate A;Reference number: JQ1409; MUID:92166764
A;Recession: JQ1419
                                                R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                                             A:Status: preliminary
A:Status: preliminary
A:Modecule type: DNA
A:Modecule type: DNA
A:Residues: 1-402 <STO>
A:Cross-references: GB:AE005174; NID:g12513857; PIDN:AAG55221.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain 0157:H7, substrain EDL933
A:Genetics:
A:Genetics:
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C;Species: barley yellow dwarf virus, BYDV
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Jun-2000
           16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A; Residues: 1-450 <MIL>
A; Cross-references: EMBL:X07653; NID:g58798; PIDN:CAA30495.1; PID:g1334818
A; Note: 422-11e was also found
C; Superfamily: potato leaf roll virus 80k protein; potato leaf roll virus c
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                                                                                                                                                                                     A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical 49.8K protein - barley yellow dwarf virus (isolate P-PAV) N'Alternate names: ORF5 protein C;Species: barley yellow dwarf virus, BYDV C;Species: barley yellow dwarf virus, BYDV C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 449;
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Pred. No. 1.2e+02;
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Pred. No. 1.4e+02;
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R; Miller, W.A.; Waterhouse, P.M.; Gerlach, W.L.
Nucleic Acids Res. 16, 6097-6111, 1988
A; Fitle: Sequence and organization of barley yellow
A; Reference number: S00946; MUID:88289355
A; Accession: S00950
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SISVSKLGGQSMQYIENEKCETK
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26.1%;
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A; Cross-ref
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R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1467, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-402 *BLATY
A; Cross-references: GB: AE000186; GB: U00096; NID:91787058; PIDN: AAC73932.1; PID:91787068;
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: cynx protein
C; Keywords: transmembrane #status predicted <TM1>
F; 52-68/Domain: transmembrane #status predicted <TM5>
F; 79-95/Domain: transmembrane #status predicted <TM6>
F; 117-187/Domain: transmembrane #status predicted <TM6>
F; 1187/Domain: transmembrane #status pr
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.4%; Score 45; DB 2; 26.1%; Pred. No. 1.2e+02; iive 16; Mismatches 1
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <STO>
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Matches
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Cidate: 31.Mar-2000 #sequence_revision 31.Mar-2000 #text_change 11-May-2000
CiAccession: E81706
Rigad T.D.; Brunham, M.; Nelson, W.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chiamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Accession: E81706
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-826 <-TETY
A;Cross-references: GB:AE002307; GB:AE002160; NID:g7190442; PIDN:AAF39264.1; PID:g719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein D1044.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
B;Pauley, A.
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A;Pauley, A;Pauley
A;Pauley, A;Pauley
A;P
               conserved hypothetical protein frameshift TC0408 [imported] - Chlamydia muridarum (st C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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A;Gene: CESP:D1044.3
A;Introns: 35/2; 63/2; 150/1; 191/3; 207/2; 405/3; 551/3; 629/1; 764/1; 933/1; 959/2;
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SLEIAQLGGISLIFAAISNPKPP 286
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Best Local Similarity
Matches 6; Conserv
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Job time: 141 sec
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A Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-687 CSTO>
A; Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07755.1; GSPDB:GN001
A; Experimental source: strain PAO1
A; Genetics:
A; Genetics:
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83100
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
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A;Reference number: A82950; MUID:20437337
A;Accession: F83100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 49/1; 91/3; 139/2; 179/2; 221/2; 270/1; 311/3; 342/2; 399/1; 481/1; 510/2; 3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-598 <GRE>
A;Cross-references: EMBL:AF067949; PIDN:AAC19238.1; GSPDB:GN00023; CESP:T10H9.5
A;Experimental source: strain Bristol N2; clone T10H9
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 17-Mar-2000
C;Accession: T33240
R;Greco, T.; Bradshaw, H.; O'Brien, D.
Submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
A;Reference number: 221306
A;Accession: T33240
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                                                                   Indels
                           Pred. No. 1.4e+02; 3; Mismatches 0;
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Pred. No. 1.9e+02;
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21.78; Pre-
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                                                                                                                                      1 SMSIARLGGXXXXXXXXXXX 23
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26.1%;
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Best Local Similarity 28.68
Matches 6; Conservative
                   Best Local Similarity 21.7 Matches 5; Conservative
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Best Local Similarity 31.85
Matches 7; Conservative
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-066-046-39
US-08-180-371-2
US-08-596-300A-7
US-08-596-300A-14
US-08-680-326-38
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                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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US-09-167-434-3
US-08-853-755-3
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                                                                                                                                                                                                                                                                                                                                                          212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                  1 SMSIARLGGXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                           BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
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Query
Match Length DB
                                                                                                                                                                                                             CHIMERA_X
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                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB s
Maximum DB s
                                                                                  OM protein
                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
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   Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 8, A Sequence 8, A Sequence 1, A Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reznikoff, William S
APPLICANT: Gorysin, Igor Y
APPLICANT: Zhou, Hong
ITILE OF INVENTIONS: System for In Vitro Transposition
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,880 FILING DATE:
PCT-US96-07795-2
PCT-US96-07796-2
US-07-832-855-2
US-09-181-706-8
US-09-459-066-8
US-09-459-066-8
US-08-910-925-1
US-08-913-940-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08850880 Patent No. 5925545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-850-880-2
         350
350
432
635
660
660
717
717
755
775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: '53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-850-880-2
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Gaps

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Length 476;

87.5%; Score 49; DB 2; 31.8%; Pred. No. 57; tive 15; Mismatches (

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dasmahapatra, Bimalendu
APPLICANT: Dasmahapatra, Bimalendu
TITLE OF INVENTION: No. 5599906el Protease Assays
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                        960296.94142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPRISE: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,901
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PROR APPLICATION 1435
PROR APPLICATION UNMER: US/08/33,901
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 13-APR-1990
APPLICATION NUMBER: 07/509,007
FILING DATE: 13-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 49;
31.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Dulak, No. 5599906man C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08333901
Patent No. 5599906
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 9602
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: alloar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MSIARLGGXXXXXXXXXXXX 23
                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.5%
Best Local Similarity 31.8%
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-814-877-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SINLL: Madison
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07940
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US-08-333-901-2
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
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Sequence 2, Application US/08814877

Sequence 2, Application US/08814877

Fatent No. 596543

GENERAL INFORMATION:

APPLICANT: Goryshin, Igor Y

APPLICANT: Reznikoff, William S

TITLE OF INVENTION: System for In Vitro Transposition

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
                                                                                                GENERAL INFORMATION:
APPLICANT: Reznikoff, William S
APPLICANT: Goryshin, Igor Y
APPLICANT: Goryshin, Igor Y
APPLICANT: Zhou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 53703

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/944,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5%; Score 49; DB 2; 31.8%; Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/850,880
FILING DATE: 02-NAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                           Sequence 2, Application US/08944916
Patent No. 5948622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 MAIARLGGFMDSKRTGIASWGA 448
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 31.8*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-944-916-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                           CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                US-08-944-916-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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amino acid

qq

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APPLICANT: Otake, Hideko
APPLICANT: Otake, Hideko
APPLICANT: Koyama, Yasuji
APPLICANT: Koyama, Yasuji
APPLICANT: Koyama, Yasuji
APPLICANT: Norano, Filchi
TITLE OF INVENTION: N-Acetylmannosamine Dehydrogenase Gene and
TITLE OF INVENTION: Productin of N-Acetylmannosamine Dehydrogenase
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
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30.0%; Pred. No. 1.9e+02;
Live 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                     Schering-Plough Corporation
                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/898,789
FILING DATE: 23-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/923,988
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: 07/924,988
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 13-APR-1990
ATTONNEY/AGENT INFORMATION:
NAME: DULAK, NO. 5894635man C.
INFORMATION FOR SEG ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07637865
Patent No. 5942427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 IARLGGDEFTFKKLIRDSGQ 201
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                                            One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.8%
Best Local Similarity 30.0%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-898-789-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1990122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
                                                               Madison
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-637-865-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                            Gaps
                                                                                                         Query Match 76.8%; Score 43; DB 1; Length 236; Best Local Similarity 30.0%; Pred. No. 1.9e+02; Matches 6; Conservative 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.8%; Score 43; DB 1; Length 236; 30.0%; Pred. No. 1.9e+02; tive 14; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dasmahapatra, Bimalendu
TITLE OF INVENTION: No. 5721133el Protease Assays
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-898-789-2
US-08-898-789-2
Sequence 2, Application US/08898789
Partent No. 5891635
GENERAL INFORMATION:
APPLICANT: Dasmahapatra, Bimalendu
TILLE OF INVENTION: No. 5891635el Protease Assays
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,582
FILING DATE: 01-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/923,988
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 11-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: DULAK, NO: 5721133man C.
                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08456582 Patent No. 5721133
                                                                                                                                                                                                                             182 IARLGGDEFTFKKLIRDSGQ 201
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
              ; MOLECULE TYPE: peptide US-08-333-901-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-582-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserve
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-456-582-2
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Patent No. 6031154
CENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Ranayama, Yoshinori
TITLE OF INVENTION: Fructokinase Genes and Their Use in
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweetness
NUMBER OF SEQUENCES: 6
CORRESPONDENCES DE CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                         APPLICANT: Donadio, S
APPLICANT: About Laboration:
APPLICANT: Acalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 one Abbott
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3170;
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26.1%; Pred. No. 1.6e+04;
Live 15; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
      5,
  6; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/439,009A
11-MAY-1995
10: 435
                                                                                                                                                                                        Sequence 5, Application US/08439009A Patent No. 6004787
                                                                   668 SRVLARLGGQGGMASFGLGTEQA 690
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                                           1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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STATE: lb
COUNTRY: US
TE: 60064-3500
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                      US-08-439-009A-5
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      Matches
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APPLICANT: Ratz, L
APPLICANT: Donadio.;
APPLICANT: Donadio. S
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park R
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3170;
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.8%; Score 43; DB 2; Length 271 Best Local Similarity 23.8%; Pred. No. 2.4e+02; Matches 5; Conservative 16; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2;
Pred. No. 1.6e+04;
                                                          NAME: Skerpon, Joseph M.
REGISTRATION NUMBER: 29,864
REFERENCE/DOCKET NUMBER: 0118.033382
TELECOMMUNICATION INFORMATION:
TELEPAN: 202-296-7500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 aniho acids
TYPE: AMINO ACID
TOPOLOGY: linear
APPLICATION NUMBER: JP 01-338267
FILING DATE: 28-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07642734C Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 3265
REFERENCE/DOCKET NUMBER: 495;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AVARLGGLDILVAGGALKGGT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SIARLGGXXXXXXXXXXX 23
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26.1%;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3170 amino acids
                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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3Y: linear
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Best Local Similarity
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Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Gelfand, Roger D.
APPLICANT: Oalhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEYR 20050 USA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

SOFTWARE: Patentin Release #1.0,

SOFTWARE: PCT-DOS/MS-DOS

SOFTWARE: PCT-DOS/MS-DOS

SOFTWARE: PCT-DOS/MS-DOS

FILING DATE: 19921014

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/800,218

FILING DATE: 29-NOV-1991

ATTONEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application PC/TUS9208756A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Limbach and Limbach STREET: 2001 Ferry Building CITY: San Francisco CONTE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: WEYR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
                                                                                                                                                                                                                                                                                          Acetobacter xylinum
                  TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERLETICS:
LENGTH: 493 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AISRLGGDEFAILLRRSLKLM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SIARLGGXXXXXXXXXXX 23
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TELEX: 278356
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 493 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                        TOPOLOGY: linear
MOLEGULE TYPE: protein
HYPOTHETICAL: NO
MATI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Acetobacter
US-08-309-512-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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PCT-US92-08756A-11
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TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
21P: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.2%; Score 41; DB 3; Length 328; 17.4%; Pred. No. 7.1e+02; tive 18; Mismatches 1; Indels
                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/826,611
FILING DATE: 05-APR-1997
CLASSIFICATION: 800
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,512
                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
RECISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-077400US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: 8145-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5759828
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Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-826-611-6
California
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-309-512-11
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73.2%; Score 41; DB 5; Length 507; 23.8%; Pred. No. 1.4e+03; tive 16; Mismatches 0; Indels
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Patent No. 6204252
GENERAL INFORMATION:
APPLICANT: MURPHY, Cheryl
STOREY, James
BELTZ, Gerald A.
TITLE OF INVENTION: CHRRACTERIZATION OF GRANULOCYTIC
FIFLE OF INVENTION: CHRRACTERIZATION OF USE
                                                                                                                           APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P450lpr Gene and Its
TITLE OF INVENTION: Uses
TUTLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/05758 FILLING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
RECISTRATION NUMBER: 30.727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEPHONE: 716-263-1600
                                                                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: P.O. Box 1051, Clinton Square CITY: Rochester STATE: New York
                                                                                   Sequence 22, Application PC/TUS9505758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CHROMOSOME/SEGMENT: Chromosome PCT-US95-05758-22
                                                                                                                                                                                                                                                                                                                                         ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: Rutgers
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 507 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Musca domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 23.8
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                  PCT-US95-05758-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-066-046-39
                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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0
                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.2%; Score 41; DB 1; Length 507; 23.8%; Pred. No. 1.40+03; Live 16; Mismatches 0; Indels
                                                                                                                                                   73.2%; Score 41; DB 5; Length 493; 23.8%; Pred. No. 1.4e+03; Live 16; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19603/240 (D-1519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: P.O. Box 1051, Clinton Square CITY: Rochester STRATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome
US-08-457-274A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DAFE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1500
                      ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter xylinum
PCT-US92-08756A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 SISKLGGLTFNELAAQVFVFF 303
                                                                                                                                                                                                                                                                217 AISRLGGDEFAILLRRSLKLM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: Rutgers
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SIARLGGXXXXXXXXXXX 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Musca domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 23.8%
Matches 5; Conservative
                                                                                                                                                                          Best Local Similarity 23.83
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 14603
COMPUTER READABLE FORM:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-457-274A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                               qq
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Gaps

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ADDRESSEE: HALE AND DORR LIP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States
ZIP: 02109
COMPUTER: United States
ZIP: 02109
COMPUTER: IDM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TOWN DATE: 24-Apr-1998
FILING DATE: 39-850
FREGISTRATION INFORMATION:
FREGISTRATION INFORMATION:
FREERENCE/POCKET NUMBER: 106.941.155
FREERENCE/COCKET NUMBER: 106.941.155
FRE
```

Query Match 73.2%; Score 41; DB 4; Length 545; Best Local Similarity 26.1%; Pred. No. 1.6e+03; Matches 6; Conservative 14; Mismatches 3; Indels 242 SFESARLGGLSVGFSYSPTGYRD 264 1 SMSIARLGGXXXXXXXXXXX 23 ογ qq

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Gaps

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Search completed: May 8, 2002, 07:29:16 Job time: 74 sec

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GenCore version 4.5 . . Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 522463 seqs, 74073290 residues
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                           1 SMSIARLGGXXXXXXXXXXXX
                                                                                                                                                                                                                                             BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                          CHIMERA_X
56
                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                      Run on:
                                                                                                                                                                           Title:
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Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1991.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1992.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1993.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1994.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1990.DAT:* A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Prostate homing an Chimeric prostatePJDB-neo-ATE trans
Modified (transpos
Mutant Tn5 transpo
Wildtype Tn5 transpo
Mutant Tn5 transpo Description Sen vis SUMMARIES AAY42537 AAY42538 AAY42539 AAY42540 AAY42541 AAR07414 AAW56694 AAB21938 AAY42535 AAY42536 a, Length DB Query 87.5 87.5 87.5 87.5 87.5 87.5 100.0 4 4 4 4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 Score Result Š

Tn5	Mutant Ins transpo Modified Ins trans	Wild-type In5 tran	Eucalyptus grandis	V coat prot	C. glutamicum SRT	C glutamicum prote	C. glutamicum SRT	BYDV coat protein	BYDV coat protein	Enterococcus faeca	Enterococcus faeca	Peptide #8460 enco	Peptide #12429 enc	Eucalyptus grandis	c glutamicum prote	C glutamicum prote	S. aggregatum PKS	Caenorhabditis ele	Caenorhabditis ele	Arabidopsis thalia	Zea mays protein f	N-acetylmannosamin	Phage lambda repre	Peptide encoded by	Amino acid sequenc	Plasmid pCSJ bacte	Plasmid pAW12/10 b	ß	S	Ø	Arabidopsis thalia
AAY42542	AAY42544 AAY15382	AAB61988	AAB32837	AAY82494	AAB78883	AAG92356	AAB78882	AAY82492	AAY82493	AAY00211	AAY00210	AAM22026	AAM38392	AAB25307	AAG89888	AAG93055	AAB10483	AAY95559	AAY95556	AAG24404	AAG25901	AAR12878	AAW47125	AAY41286	AAW80738	AAW58897	AAW58895	AAG30797	AAG30796	AAG39232	AAG39231
200	202	22	71	21	22	22	22	21	21	20	20	22	22	21	22	22	21	21	21	21	21	12	19	20	19	19	19	21	21	21	21
476	476	476	142	382	389	484	484	651	724	1416	1448	109	109	166	268	314	1622	2870	3178	133	162	231	236	236	237	237	237	247	248	252	253
87.5	87.5	87.5	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	8.9/	76.8	76.8	76.8		٠	•	•			8.92	•
44 0 0 0	4 4 0 0	49	45	45	45	45	45	45	45	45	45	44	44	44	44	44	44	44	44	43	43	43	43	43	43	43	43	43	43	43	43
13	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	. 36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

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Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
                                                                                                                                                                                                                                                                                                                    Pasqualini R, Ruoslahti EI;
                                                                       Prostate homing antimicrobial pro-apoptotic conjugate.
                                                                                                                                                                  Key Location/Qualifiers
Misc-difference 10..23 /note= "Preferably D-form residues"
         Ä
        AAB21938 standard; Peptide; 23
                                                                                                                                                                                                                                                       21-JAN-2000; 2000WO-US01602.
                                                                                                                                                                                                                                                                           99US-0235902.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       Ellerby HM, Bredesen DE,
                                                                                                                                     Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                 (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                           WPI; 2000-499174/44.
                                                                                                                                                                                                              WO200042973-A2
                                                                                                                                                                                                                                                                           22-JAN-1999;
                                                 22-MAR-2001
                                                                                                                                                                                                                                  27-JUL-2000.
                             AAB21938;
AAB21938
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                                                                                                                  comprising of a tumour homing molecule that selectively homes to a mammaalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammaalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcomabreast and prostate cancer or melanoma. The present sequence is one such prostate homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
            Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                    The present invention relates to homing pro-apoptotic conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellerby HM;
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                                                                                                                                                                                                                                                                                                                                 DB 21; Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Coupling_domain
/note= "Glycinylglycine bridge"
10..23
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Prostate_homing_domain
                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 2
                                                                                                                                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                       Claim 29; Page 108; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                          1 SMSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE06513 standard; peptide; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ď,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000US-0489582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasqualini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BURN-) BURNHAM INST.
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                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                   23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153342-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruoslahti EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE06513;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE06513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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The DNA sequence encoding this sequence (together with 4 others, see AAR07413 and AAR08165-67) contains the Neo structural gene or its deriv. with, except for the region upstream of the translation initiation codon, and the translation initiation codon itself, 7 additional ATG sequences present. A plasmid contg. this sequence can also comprise a promoter. The combination of plasmids having different expression powers, results in various kinds of regulatory sequences having different expression capacities which can be measured quantitatively. See tag b of AAQ06275.
                                          The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a chimeric
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector; regulatory sequence; plasmids; expression; ATG codon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vector for detection of regulatory sequence - by using combination of plasmids with different expression powers etc.
                                                                                                                                                                                                                                                                                       Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 49;
                                                                                                                                                                                                                                                                                                                        Indels
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0
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                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                       100.0%; Score 56; DB 2 39.1%; Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.5%; Score 49; DB Best Local Similarity 31.8%; Pred. No. 5.6; Matches 7; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                      prostate-homing pro-apoptotic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pJDB-neo-ATE translation product 2.
            Claim 6; Page 103; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                            1 SMSIARLGGXXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR07414
ID AAR07414 standard; protein; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter; Neo structural gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89JP-0041604.
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                                                                                                                                                                                                                                                                                                                          9; Conservative
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                     23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1990,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is a modified Th5 (transposon 5) transposase enzyme sequence that has both greater avidity for Th5 outside end (OE) repeats and is less likely to assume an inactive multimeric form than a wild type Th5 transposase. This can be used in the construction of novel genetic constructs which comprise this Th5 transposase encoding nucleotide sequence and a transposable DNA sequence flanked at its 5' and 3' ends by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A at position 10, T at 11 and A at 12. The modified Th5 transposase and the transposable DNA which is a DNA donor molecule are used in a system for in vitro transposition. The system and method can be used to create absolute defective mutants, to provide selective markers to target DNA, to forcible regions of homology to a target DNA, to facilitate insertion of specialised DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequencing, to facilitate production of genetic fusion for gene expression studies and protein domain mapping, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 well as to bring together other desired combinations of DNA sequences (combinatorial genetics). The modified Tn5 transposase facilitates in vitro transposition reaction rates of at least about 100-fold higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified Tn5 transposase construct used in novel system for in vitro transposition - used to, e.g. create absolute defective mutants, provide selective markers and to facilitate insertion of specialised DNA sequences into target DNA
                                                                                                                                                                                                                                                                                           Tn5 transposase; modified; enzyme; in vitro transposition; mutant; target; marker; transposon 5.
                                                                                                                                                                                                                                                                                                                                                                                                                              /label- E54K
/note- "wild type Glu is replaced by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild type Leu is replaced by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "wild type Met replaced by Ala"
                                                                                                                                                                                                                                                          Modified (transposon 5) In5 transposase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pages 31-33; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou H;
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                           AAW56694 standard; Protein; 476 AA.
                                     26 maiarlggfmdskrtgiaswga 47
             2 MSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- L372P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= M56A
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96US-0814877
                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 54
                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV28397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1997;
                                                                                                                                                                                                                    24-JUL-1998
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                                                                                                                                                                               AAW56694;
                                                                                                                          AAW56694
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This sequence represents mutant Tn5 transposase EK54 MA56 LP372. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avoidity than the wildtype Tn5 transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure. The improved avidity of the modified transposase for the regeat sequences for the outside End (DE) terminic is due to the Lys residue at amino acid 54, which is Glu in wild type Tn5 transposase (AAV42536). The mutation strongly alters the preference of the transposase (AAV42536). The mutation strongly alters the preference to the higher binding of this mutation, known as EK54, to DE termini. The higher binding of this mutation, known as EK54, to DE termini. The higher binding of this mutation, known as EK54, to DE termini results in a transposase. Similar changes at position 54 to val and position 47 (Thr to Pro change) also result in increased binding to the DE termini. The reduction in the formation of the inactive mutimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Th5 transposase to Pro (LP372). This sequence also has a substitution of translation of an inhibitor protein, the initiation codon of which
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than can be achieved using wild type transposase (as measure in vivo). In vitro transposition using this system can also use donor DNA and target DNA that is circular or linear. The system also requires no outside high energy source and no other protein other than the modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transposase; modified form; wildtype; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                          87.5%; Score 49; DB 19; Length 476; 31.8%; Pred. No. 1.4e+02; ive 15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42535 standard; Protein; 476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 maiarlggfmdskrtgiaswga 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 MSIARLGGXXXXXXXXXXX 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                  476 AA;
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Synthetic.
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                                                                                                                                                               ransposase
                                                                                                                                                                                                                                      Sequence
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                                                                                                                                    transposase enzyme is useful in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to facilitate insertion of specialised DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequencing, and to facilitate production of genetic fusions for gene expression studies and protein domain mapping.
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                           mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. The mutant
corresponds to the sequence encoding wildtype Met 56. As a result, the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 49; DB 20; Length 470
31.8%; Pred. No. 1.4e+02;
... ...marrhes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 maiarlggfmdskrtgiaswga 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wildtype In5 transposase.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            476 AA;
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char42538, AAY42540) and position 47 (Thr to Pro change, TP47, AAY42542))

also result in increased binding to the OE termini. Mutants with a also result in increased binding to the OE termini. Mutants with a substitution of Ala for wildtype Met at position 5 exhibited a higher transposition rate than the wildtype. This substitution prevents the transposition of an inhibitor protein, the initiation codon of which corresponds to the sequence encoding wildtype Met 56. The Th5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Th10-based systems. The mutant transposase enzyme is useful in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective markers to rarget DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences can to target DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences can be present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified transposase enzyme for use in a system for introducing genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%; Score 49; DB 20; Lk
31.8%; Pred. No. 1.4e+02;
ive 15; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 MSIARLGGXXXXXXXXXXX 23
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             476 AA;
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is due to the Lys residue at amino acid 54, which is Glu in wild type Transposase (AAV42536). The mutation strongly alters the preference of the transposase (Control of the Inside End (IE) termini. The higher binding of this mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini results in a transposaic. The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Tn5 transposase to Pro (LP372). The Tn5-based transposation system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. The modified transposase enzyme setul in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to provide primer binding sites or tags for DNA sequencies and protein domain mapping.
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                                                                                                                                                                                                                                                                                                                                                      derived from the mutant Tn5 transposase sequence given in columns 15-18,
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                                                                                                                                                                                                                                                                                                                                     present sequence is not shown in the specification but is
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                        87.5%; Score 49; DB 20; Length 47t
31.8%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY42538 standard; protein; 476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant In5 transposase EV54 LP372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 31.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         476 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Transposace for the repeat sequences for the Outside End (OE) terminicated transposace (AAY4236). The mutation strongly alters the preference of the transposace (AAY4236). The mutation strongly alters the preference of the transposace for the OE termini, as opposed to the Inside End (IE) termini results in a transposace for the sequence of the transposace for the a transposace. The reduction in the formation of the termini results in a transposace. The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (Leu) of wildtype Transposace to Pro (LB72). The Tr5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. The modified transposace enzyme is useful in a system for introducing genetic changes to nucleic acid. The method can be applied to create absolute defective mutants, to provide selective narkers to target DNA, to provide portable regions of homology to a target DNA, to provide primer binding sites or tags for DNA sequencing, and to facilitate production of specialised DNA sequencing, and to facilitate insertion of specialised DNA sequencing, and to facilitate domain mapping.

Note: The present sequence is not shown in the specification but is columns 15-18.
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inactive multimeric structure. The improved avidity of the modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%; Score 49; DB 20; Length 476; 31.8%; Pred. No. 1.4e+02; ive 15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MSIARLGGXXXXXXXXXXX 23
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Best Local Similarity 31.85
Matches 7; Conservative
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changes to nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                            476 AA;
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seen with wild-type transposase. The In5-based transposition
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     transposase. The improved avidity of the modified
transposase for the repeat sequences for the Outside End (OE) termini
sis due to the Lys residue at amino acid 54, which is Glu in wild type
The transposase (AAY4236). The mutation strongly alters the preference
of the transposase for the OE termini, as opposed to the Inside End (IE)
termini. The higher binding of this mutation, known as ERS4, to OE
termini results in a transposition rate that is about 10-fold higher
system is more broadly applicable and utilises shorter, more well
defined termini that are active on DNA of any structure when compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents mutant Tn5 transposase EV54. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater aviality than the wildtype Tn5 transposase. The improved aviality of the modified transposase for the repeat sequences for the Outside End (OE) terminis due to the Val residue at amino acid 54, which is Glu in wild type Tn5 transposase (AAYA2536). The mutation strongly alters the preference of the transposase for the OE termini, as opposed to the Inside End (IE) termini. The higher binding of this mutation, known as EV54, to OE termini results in a transposition rate that is about 3-fold higher than
                                                                                                                                                           Note: The present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                                                                                     Gaps
 sequences of donor DNA with greater avidity than the wildtype Tn5
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                                                                                                                                                                                                                                        87.5%; Score 49; DB 20; Length 476; 31.8%; Pred. No. 1.4e+02;
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15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                            427 maiarlggfmdskrtgiaswga 448
                                                                                                                                                                                                                                                                                             2 MSIARLGGXXXXXXXXXXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Tn5 transposase EV54
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                                                                                                                                                                                                                                                                    7; Conservative
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                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                            derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transposase, modified form, wildtype, mutant; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutein.
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                  Note: The present sequence is not shown in the specification but is
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system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when comp. Mu- and Tn10-based systems.
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                                                                                                                                                                                                                  Score 49; DB 20; Length 4.7.
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                 87.5%;
31.8%;
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Best Local Similarity 31.8%
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AAY42542;

AAY42542

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This sequence represents mutant Tn5 transposase MA56. This sequence has a substitution of Ala for wildtype Met at position 56. This substitution prevents the translation of an inhibitor protein, the initiation codon of which corresponds to the sequence encoding wildtype Met 56. As a result, the mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified transposase enzyme for use in a system for introducing genetic changes to nucleic acid \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                active on DNA of any structure when compared to Mu- and Tn10-based
                                                                                                                                                            Transposase; modified form; wildtype; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutant; mutein.
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AAY42543 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WISC ) WISCONSIN ALUMNI RES FOUND.
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                                                                                                                         Mutant In5 transposase MA56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goryshin IY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.8<sup>†</sup>
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents mutant Tn5 transposase TP47. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avidity than the wildtype Tn5 transposase. The improved avidity of the modified transposase for the repeat sequences for the Outside End (OE) terminity of the modified transposase for the repeat sequences for the Outside End (OE) terminity of the transposase for the OE terminity as opposed to the Inside End (IE) terminity. The higher binding of this mutation, known as TP47, to OE terminity The higher binding of this mutation, known as TP47, to OE terminity and transposition rate that is about 10-fold higher than seen with wild-type transposase. The Tn5-based transposition defined terminity that are active on DNA of any structure when compared to when compared to the transposase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The present sequence is not shown in the specification but is derived from the mutant In5 transposase sequence given in columns 15-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified transposase enzyme for use in a system for introducing genetic
                                                                                                                                                                                                                                                                                                                               Transposase; modified form; wildtype; mutant; multimeric; OE termini; IE termini; outside end termini; inside end termini; repeat sequence; mutation; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%; Score 49; DB 20; Length 47
31.8%; Pred. No. 1.4e+02;
ive 15; Mismatches 0; Indels
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                                                                                                                                                              AAY42542 standard; protein; 476 AA.
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                                       427 maiarlggfmdskrtgiaswga 448
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                 2 MSIARLGGXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                          4utant In5 transposase TP47
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Best Local Similarity 31.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Transposon Tn5.
Synthetic.
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Gaps

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Transposon In5.

Sequence

RESULT 13 AAY42543

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97US-0944916. 97US-0944916. 97US-0850880

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Goryshin IY, Reznikoff WS, York DL, Zhou H;
                                                                                                                                                                                                        (WISC ) WISCONSIN ALUMNI RES FOUND.
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                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ06433
                                                                   06-OCT-1997;
                                                                                                             06-OCT-1997;
                                                                                                                                                         02-MAY-1997;
                       07-SEP-1999
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    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents mutant Tn5 transposase EK54 MA56. This mutant form differs from the wildtype in that it binds to repeat sequences of donor DNA with greater avidity than the wildtype Tn5 transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure. The improved avidity of the modified transposase for the repeat sequences for the Outside End (OE) termini; so due to the Lys residue at amino acid 54, which is Glu in wild type Tn5 transposase (AAY42536). The mutation strongly alters the preference of the transposase (or the OE termini, as opposed to the Inside End (IE) termini. The higher binding of this mutation, known as EK54, to OE termini. The higher binding of this mutation, known as EK54, to OE termini. The higher binding of this mutation, shown as EA54, to OE termini results in a transposition rate that is about 10-fold higher than seen with wild type transposase. This sequence also has a substitution of Ala for wildtype whet at position 56. This substitution prevents the translation of an inhibitor protein, the initiation codon of which corresponds to the sequence encoding wildtype Met 56. As a result, the mutant transposase exhibits a somewhat higher transposition rate. The Tn5-based transposition system is more broadly applicable and utilises shorter, more well defined termini that are active on DNA of any structure when compared to Mu- and Tn10-based systems. Note: The present sequence is not shown in the specification but is derived from the mutant Tn5 transposase sequence given in columns 15-18.
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                                                                                                                                                                                                                                                                                                                                                          Modified transposase enzyme for use in a system for introducing genetic changes to nucleic acid \dot{\mathbf{c}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 49; DB 20; Length 476;
; Pred. No. 1.4e+02;
15; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page -; 21pp; English.
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Best Local Similarity 31.55
Best Local 7; Conservative
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Synthetic.
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This is the amino acid sequence containing the modified form of the transposase enzyme. This modified form differs from the wildtype in that it binds to the repeat sequences of the donor DAR with greater avidity than the wildtype TTS transposase and it is less likely than the wildtype TTS transposase and it is less likely than the wildtype protein to assume an inactive multimeric structure. The improved avidity of the modified transposase for the repeat sequences for the Outside End (OE) termini (class (1) mutation) can be achieved by providing a lysine residue at amino acid 54, which is achieved by providing a lysine residue at amino acid 54, which is the preference of the transposase for the OE termini, as opposed to the Inside End (IE) termini. The higher binding of this mutation, known as the preference of the transposase for the OE terminis about 10-fold higher than seen with wild type transposase. Similar changes at position 54 to valine and position 47 (threonine-to-proline change) also result in increase binding to the OE termini. The reduction in the formation of the inactive multimeric form is achieved by modifying amino acid 372 (leucine) of wildtype TN5 transposase to a proline (class (2) mutation, LP372). The TN5-based transposition system is more broadly applicable and the transposition system is more broadly applicable and the transposition system is more broadly applicable and the transposition system is more broadly applicable on the transposition of the more broadly applicable and the transposition system is more broadly applicable and the transposition and the province the province transposition and the prov
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In vitro transposition using a In5 based genetic construct
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31.8%; Pred. No. 1.4e+02;
ive 15; Mismatches 0;
                                                                                                                  Disclosure; Column 27-31; 48pp; English.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

May 8, 2002, 07:18:34; Search time 38.66 Seconds Run on:

(without alignments)
13.412 Million cell updates/sec

us-69-765-086-207

30 1 SMSIARL 7 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_1101:* Database :

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score		March Length DB ID 100.0 7 20 AP 100.0 7 21 AP 100.0 23 21 AP 100.0 23 22 AP 96.7 256 22 AP 90.0 191 21 AP 90.0 289 22 AP 86.7 183 22 AP	22 22 22 22 22 22 22 22 22 22 22 22 22	AAY48905 AABZ1907 AABZ1938 AABZ1938 AABZ1938 AABZ1938 AAGS1999 AAY37469 AAJ14174	Membrane dipeptida Membrane dipeptida Human prostate-hom Mouse prostate-hom Prostate homing an Chimeric prostate- C qlutamicum prote Arabidopsis thalia C glutamicum prote Protein involved i Human novel protei
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AAG92195	AAW18032	AAB25565	AAM4 0225	AAG98415	AAG98916	AAG98948	AAY75241	AAG92942	AAB39477	AAB94277	AAW20100	AAW98839	AAG04867	AAG42777	AAG04866	AAG42776	AAG04865	AAG42775	AAG21936	AAG21935	AAG21934	AAR62448	AAR62447	AAB07564	AAB27643	AAR07414	AAB44338	AAG55635	AAG58828	AAM14873	AAM27300	AAM02598
22	18	21	22	22	22	22	21	22	21	22	18	19	21	21	21	21	21	21	21	21	21	15	15	21	21	11	21	21	21	22	22	22
382	422	697	748	118	118	118	204	381	64	120	137	266	319	319	336	336	342	342	363	381	387	477	515	2675	23	49	62	63	63	81	81	81
86.7	86.7	86.7	86.7	83.3		83.3	83.3	83.3	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0		80.0	80.0	80.0	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7
26	7 7 7 8	26	56	25	25	25	25	25	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	23	23	23			23	23	23
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ALIGNMENTS

AAY48905 standard; Peptide; 7 AA. (first entry) 10-DEC-1999 AAY48905;

AAY48905 RESULT

Membrane dipeptidase-binding prostate homing peptide #21.

Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.

Homo-sapaens. W09946284-A2 Synthetic

99WO-US05284 10-MAR-1999; 6-SEP-1999

98US-0042107. (BURN-) BURNHAM INST 13-MAR-1998; 26-FEB-1999;

Pasqualini R, Rajotte D,

Ruoslahti EI;

WPI; 1999-571717/48.

New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological

Gaps

; 0

Indels

Length 7;

Score 30; DB 21; Pred. No. 4.3e+05;

100.0%; 100.0%;

7 AA;

0; Mismatches

(first entry)

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Mouse, chimeric prostate-homing pro-apoptotic peptide;
prostate-homing peptide; antimicrobial peptide; prostate cancer;
tumour homing molecule; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse prostate homing peptide #1.
                                                                                                                                                                                                                                                                               AAE06483 standard; peptide; 7 AA.
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                                                                    The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a tranget molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and Iymph node. The peptide bind to the membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; Page 107; 118pp; English.
                                     Claim 1; Page 151; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB21907 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate-homing peptide #1.
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7; Conservative
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conditions
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                                                                                                                              Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an
Ellerby HM;
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DE,
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   Bredesen
Arap W,
                                                                                                                                                                                                                                                        Claim 2; Page 103; 176pp; English.
Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugates of the invention.
                                                                                                                                                                                             antimicrobial peptide
                                                           WPI; 2001-451901/48.
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smsiarl 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to anglogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such prostate homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
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                                                                                                                                          Prostate homing antimicrobial pro-apoptotic conjugate.
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Misc-difference 10..23 /note= "Preferably D-form residues"
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                   AAB21938 standard; Peptide; 23 AA.
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Matches 7; Conservative
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Chimeric - Unidentified
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AAB21938
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucled acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                    Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                      Claim 17; SEQ ID NO: 4337; 246pp + Sequence Listing; English.
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85.7%; Pred. No. 13;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 6694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG08955 standard; Protein; 191 AA.
                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                       07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                            18-DEC-2000; 2000EP-0127688
                                                                                                           99JP-0377484
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                               WPI; 2001-376931/40.
N-PSDB; AAH65802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA;
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              EP1108790-A2.
                                                                                                                                                                                                    Nakagawa S,
Tateishi N,
                                           20-JUN-2001
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PR 13-7UL-1999 99US-0143277

PR 13-7UL-1999 99US-014322

PR 15-7UL-1999 99US-014322

PR 15-7UL-1999 99US-014422

PR 15-7UL-1999 99US-014422

PR 19-7UL-1999 99US-014423

PR 19-7UL-1999 99US-014423

PR 19-7UL-1999 99US-014423

PR 20-7UL-1999 99US-014433

PR 20-7UL-1999 99US-014433

PR 20-7UL-1999 99US-014433

PR 21-7UL-1999 99US-014508

PR 22-7UL-1999 99US-014958

PR 22-7UC-1999 99US-014958

PR 23-7UC-1999 99US-014958

PR 23-7UC-1999 99US-014958

PR 23-7UC-1999 99US-014958

PR 23-7UC-1999 99US-014958

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 21; Length 191;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C glutamicum protein fragment SEQ ID NO: 5753.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG91999 standard; Protein; 289 AA
990S-0157117.
990S-0157753.
990S-0157865.
990S-0158029.
990S-01583369.
990S-01593369.
                                                                                99US - 0.159294
99US - 0.159329
99US - 0.159330
99US - 0.159331
99US - 0.159637
99US - 0.159638
99US - 0.159634
99US - 0.160741
99US - 0.160770
99US - 0.160770
99US - 0.160814
99US - 0.160814
99US - 0.160814
99US - 0.160814
99US - 0.160819
99US - 0.160819
99US - 0.160819
99US - 0.160819
                                                                                                                                                                                                                                                                                                                                 990S-0161360
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%;
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 6; Conservative
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|12 smaiarl 18
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                                                                                                                                                                                        1-OCT-1999;
1-OCT-1999;
1-OCT-1999;
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1-0CT-1999;
2-0CT-1999;
2-0CT-1999;
2-0CT-1999;
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29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG91999;
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AAG91999
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Disclosure; Page 1157-1158; 1755pp; English.
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                                                                                                                                          sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                 mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                        for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                  The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                           Claim 17; SEQ ID NO: 5753; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein involved in intermediate metabolism of polypeptides.
                                                                                                                                                                                                                                                                                                                         DB 22; Length 289;
50;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                       polynucleotides derived from Coryneform bacteria,
                                                                                                                                                                                                                                                                                                                                               Mismatches
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                         Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY37469 standard; Protein; 301 AA.
 Ikeda M,
                                                                                                                                                                                                                                                                                                                         90.0%;
85.7%;
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                    European Patent Office.
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 Senoh A,
                     WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-371125/31.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                         289 AA;
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142 smsiarv 148
                                N-PSDB; AAH67218
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17-DEC-1997;
 Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY37469;
                                                                                                                                                                                                                                                                                          Sequence
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                                                       Novel
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AAX36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye plaseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genttal diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and venerallymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; vulnerary; nootropic; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 301;
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Pred. No. 52;
1; Mismatches
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52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   301 AA;
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|158 smaiar| 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SMSIARL 7
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polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bours, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporasis and osteoarthitis, as an Alzhelmer's, Parkinson's and Huntington's diseases, amylotrophic lateral scalers; stroke, immune deficiencies resulting from bacterial, viral or fermine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antidianemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malarta, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                      sclerosis, stroke, immune deficiencies resurcing context, asthma, fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
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Pred. No. 55;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||| ||
36 smsitr1 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-0CT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB41860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; heaptorcopic; outnearry; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimilant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; antidianed vith an ORFX-associated disorder. The presence of or predisposition to, or preventing or treating pathological conditions and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, collection, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic caneamia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antidifammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                     Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 21; Length 260;
Pred. No. 80;
2; Mismatches 0; Indels
                                                                         useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum protein fragment SEQ ID NO: 5949.
                                                                                                                                 Claim 11; Page 2449-2450; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG92195 standard; Protein; 382 AA.
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71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000JP-0159162.
2000JP-0280988.
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Best Local Similarity 71.4v
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organic acid synthesis.
WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AA;
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Tateishi N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG92195;
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                                                                                                                    The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                              ö
                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; monproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum SMP protein sequence SEQ ID NO:46.
                                                                                               Claim 17; SEQ ID NO: 5949; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                    86.7%; Score 26; DB 22; Length 382; 71.4%; Pred. No. 1.2e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB79265 standard; Protein; 382 AA.
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99DE-1031413.
99DE-1031419.
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99DE-1031424.
99DE-1031428.
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99DE-1031434.
99DE-1031510.
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                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                          European Patent Office.
 WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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192 amsvarl 198
           N-PSDB; AAH67414
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (II) or host cells containing them are used to map genomes of organisms related to nevolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 207-208; 1246pp; English.
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                                                                                                                                                                         99DE-1042076.
99DE-1042079.
99DE-1042086.
99US-0143208
99DE-1032924
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                                                            99DE-1032973
                                                                                          99DE-1033005
                                                                                                                      99DE-1040765
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pompejus M, Kroeger B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-061975/07
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                                                                                                                   27-AUG-1999
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                                                                                                                                                                                                                                         03-SEP-1999
                                                         14-JUL-1999
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(first entry)

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Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals \dot{\,}
                                                                                                               Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signaling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                            Eucalyptus grandis cell signalling involved protein SEQ ID NO:940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 518-519; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                          11-JAN-2000; 2000WO-US00724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-476052/41.
                                                                                                                                                                                                             Eucalyptus grandis.
                                                                                                                                                                                                                                                WO200042171-A1.
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                                         27-NOV-2000
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   AAB25565;
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   Isolated retinoid X receptor protein - having amino acid insert in ligand binding domain, useful to identify specific target genes implicated in retinoid responses important in disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel retinoid X receptors RXR delta (AAW18032) and RXR epsilon (AAW18033) exhibit a high degree of amino acid conservation with other vertebrate RXRs but represent unique subtypes defined by an additional 14-amino acid segment in their ligand binding domains. These RXRs do not bind 9-cis retinoic acid (RA) or all-trans RA with high affinity and are not activated by 9-cis RA. They are able to form dimers in a manner equivalent to other RXRs. Their amino acid sequences were deduced from CDNA clones (AAY67196-97) obtd. from adult and post somitogenesis zebrafish cDNA libraries. The RXRs can be used to identify ligands, isolate mammalian counterparts, modify retinoid activity and identify target genes implicated in retinoid responses important in disease states.
                                                                                                                                                                                                                                                                                 /note= "hinge between DNA-binding and ligand-binding domains"
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                                                                                                                                                                                                                                                                                                                                        /label= E
/note= "ligand-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "14-amino acid insert"
                                                                                                                                                                                                         /label= C
/note= "DNA-binding domain"
                                                                                                                                  1..89
/label= A/B
/note= "N-terminal domain"
900..156
                                       Retinoid X receptor; RXR delta; zebrafish
Zebrafish retinoid X receptor RXR delta.
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 23-25; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TOOH ) UNIV QUEENS KINGSTON.
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Best Local Similarity
Matches 5; Conserv
                                                                            Brachydanio rerio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1996;
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                                                                                                                                  Domain
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99US-0228986. 99US-0162866.

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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Phnus radiata also known as Wonterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism: Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance consecutions can be used to delay senescence in selected cell types or modifications can be used to delay senescence in selected cell types or can providing fruit and vegetables which have a longer shelf life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between harvest and consumption, or to decrease branching frequency ir forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.3e+02;
2; Mismatches 0; Indels
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Similarity 71.4%;
5; Conservative ;
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Best Local Similarity
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Job time: 48 sec

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RESULT 15 AAB25565

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
PCT-US94-12550-48
PCTT-US96-10041-26
US-08-723-306-23
PCT-US96-10041-23
US-07-908-455A-4
US-08-434-120-30
US-08-434-120-90
US-08-434-120-90
US-08-45-325-88
US-08-45-325-88
US-08-45-735-88
US-08-45-735-88
US-08-45-735-88
US-08-45-735-88
US-08-45-735-88
US-08-45-735-88
US-08-45-735-48
US-08-457-798-24
US-08-505-486-24
US-08-657-798-24
US-08-657-798-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMETAL TINFORMATION:
APPLICANT: MCLAUGhlin, Mark L
APPLICANT: MCLAUGhlin, Mark L
APPLICANT: MCLAUGhlin, Mark L
APPLICANT: MCLAUGhlin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STREET: D. O. Box 2471
CITY: Baton Rouge
STREET: LA
COUNTRY: USA
LIP: 70821-2471
COMPLER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/232,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6. Application US/08944133
Patent No. 5789542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: At TELECOMMUNICATION: TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33451
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ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 334:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 346-8049
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          2223333111111222233311
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US-08-944-133-6
      Query Match
      (without alignments)
15.190 Million cell updates/sec
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                                                                                                                                                                                                                            May 8, 2002, 07:17:52; Search time 20.74 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/laa/fg_COMB.pep:*
/cgn2_6/ptodata/2/laa/fg_COMB.pep:*
                                                                  Compugen Ltd
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US-08-465-325-86
US-08-231-730A-40
US-08-457-171-40
US-08-505-486-45
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US-08-801-028-45
US-09-340-154-45
US-09-232-802A-40
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US-08-944-133-4
US-08-944-133-8
US-08-944-133-27
US-08-944-133-25
US-08-723-306-27
US-08-723-306-27
US-08-723-306-27
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PCT-US95-09339-45
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US-07-908-455A-62
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                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM protein – protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                       US-09-765-086-200
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Maximum DB seq length: 200000000
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Match
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Sequence:
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MEDION TIPE: FLOPPY ULSA
COMPUTER: PETCHIN RELEASE #1.0, Version #1.25
SOFTWARE: PATCHIN Release #1.0, Version #1.25
SOFTWARE: PATCHIN BATA:
APPLICATION NUMBER: US/08/944,133
FLING DATE: 06-CCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-APR-1994
APPLICATION NUMBER: US/08/23,525
FILING DATE: 22-APR-1994
APPLICATION NUMBER: US/08/23,525
FILING DATE: 34-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUNNELS, John H
REGISTRATION NUMBER: Atty File No. 5789542 9301
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 1; Length 21; 100.0%; Pred. No. 0.0042; Live 0; Mismatches 0; Indels
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ZIF: 70821-2471
COMPUTER RRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-944-133-26
; Sequence 26, Application US/08944133
; Patent No. 57893-26
; GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: McLaughlin, Mark L
TITLE OF INVENTION:
CORRESPONDENCES: 54
; CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STAREE: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
                                 TITLE OF INVENTION: Amphipathic Peptides
                                                          NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. BOX 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-944-133-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLAKLAKKLAKLAK 14
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STATE: LA
COUNTRY: USA
ZIP: 70821-247
ZONFURY: USA
ZONFURY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Defortion DATA:
APPLICATION NUMBER: US/08/44/133
FILING DATE: 06-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/681,075
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE: 22-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUNNELS, JOHN H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
PELECOMMUNICATION INFORMATION:
PAGGINATION INFORMATION:
PAGGIN
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Pred. No. 0.0029;
                                                                                                                                                                                                                                                                 RESULT 2
US-08-944-133-3
Sequence 3, Application US/08944133
Sequence 3, Application US/08944133
PRACE NO. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN H. Runnels
STREET: P. O. BOX 2471
CONTY: Baton Rouge
                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McLaughlin, Mark L
                              Best Local Similarity 100.0%;
Matches 14; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                    1 KLAKLAKKLAKLAK 14
                                                                                                                                                     1 KLAKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KLAKLAKKLAKLAK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 1; Length 28; 100.0%; Pred. No. 0.0054; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Runnels, John H
REGISTRATION NUMBER: 33451
RECISTRATION NUMBER: 3451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 70821-2471

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,133

FILING DATE:

APPLICATION NUMBER: 08/789,077

FILING DATE:

APPLICATION NUMBER: US/08/681,075

FILING DATE:

CLASSIFING DATE:

APPLICATION NUMBER: US/08/681,075

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08944133;
Patent No. 5789542;
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L.
APPLICANT: Becker, Calvin L.
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
504 387-3221
                     TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 28 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                            single
                                                                                                                                           TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-944-133-4
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                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
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    TELEPHONE:
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FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEPHONE: 504 387-3221
INFORMATION FOR SEQ ID No. 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 70821-2411
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-0CT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 62; DB 1;
; Pred. No. 0.0042;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
ETLING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
  US/08/944,133
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100.0%;
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REGISTRATION NUMBER: 33451
             CLASSIFICATION: 5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-944-133-26
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Batc
STATE: LA
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Sequence 27, Application US/08723306
Patent No. 3856178
GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Morrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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POPEMALING SISTEM

PRESENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,133

FILING DATE: 06-OCT-1997

CLASSIFICATION: 5530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/681,075

FILING DATE: 03-FEB-1997

APPLICATION NUMBER: US/08/681,075

FILING DATE: US-APR-1994

ATTORNEY-AGENT INFORMATION:

NAME: RUNDELS, John H

REGISTRATION NUMBER: 33451

REFERENCE/POCKET NUMBER: 33451

REFERENCE/POCKET NUMBER: 33451

REFERENCE/POCKET NUMBER: 346-8049

INFORMATION INFORMATION:

TELEPHONE: 504 387-3221

INFORMATION FOR SEC ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
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0.014;
thes 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                         COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OMPUTER: IBM PC COMpatible
SYSTEM: PC-TOSS/MS-DOS
OPERATING SYSTEM: PC-TOSS/MS-DOS
              ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.9
Best Local Similarity 100.
Matches 13; Conservative
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                                                                                              us-us-944-133-27
Sequence 27, Application US/08944133
Patent No. 578942
GENERAL INFORMATION:
APPLICANT: McLaughlin Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
IF: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATON NUMBER: US/08/944,133
FILING DATE: US-1997
CLASSIPICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/681,075
FILING DATE:
ADDITONATOR:
APPLICATION NUMBER: US/08/681,075
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: US/08/232,525
APPLICATION NUMBER: US/08/232,525
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REGISTRATION NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18797321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08944133
Sequence 25, Application US/08944133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                   1 KLAKLAKKLAKLAK 14
                                        1 KLAKLAKKLAKLAK 14
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Gaps

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APPLICATION NUMBER: US/08/723,306

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GENERAL INFORMATION:
APPLICANT: White Phb, Kenneth
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application PC/TUS9610041
GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: Worrey PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
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                    Length 23;
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                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
FILING DATE:
CLASSIFICATION:
                  Score 57; DB 2;
Pred. No. 0.022;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
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Pred. No. 0.022;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Trask Britt and Rossa STREET: P.O. Box 2550
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Swelgert PhD, Susan E
REGISTRATION NUMBER: 254
REFERENCE/POCKET NUMBER: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 8015321922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.9%;
                  91.9%;
ilarity 92.9%;
Conservative
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LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 2550
CITY: Salt Lake City
STATE: Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 KLKKLAKKLAKLAK 21
                                                                                                  1 KLAKLAKKLAKLAK 14
                                                                                                                       8 KLKKLAKKLAKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLAKLAKKLAKLAK 14
                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                       PCT-US96-10041-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                      RESULT 11
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APPLICANT: White PhD, John
APPLICANT: Morrey PhD, John
APPLICANT: Meed, William
TITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 2; Length 23;
Pred. No. 0.022;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/08723306 Patent No. 5856178 GENERAL INFORMATION:
                               ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015319168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TXPE: amino acids
TXPE: amino acids
TXPE: amino acids
TXPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sweigert Phb. Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015319122
TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       91.9%;
92.9%;
                                                                                                                                                                                                                                                                                 not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                 ; TOPOLOGY: not relevar
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-723-306-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide; HYPOTHETICAL: YES US-08-723-306-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLAKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H HILIHIHH 8 KEKKLAKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 13; Conserv
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84110
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STATE: Ut
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps
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APPLICANT: Baker, Mangaret A.
APPLICANT: Jacob, Leonard S.
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: Treatment of Gynecological
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: MALOR STEWART
STREET: 6 ADDRESSE STEWART
STREET: 6 BECKER FARM ROAD
CITY: Roseland
STATE: NOW JURSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 1;
Pred. No. 0.053;
4; Mismatches
             FILING DATE: 15-APR-1991
APPLICATION NUMBER: US 07476629
FILING DATE: 08-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-122
RELECOMMUNICATION INFORMATION:
TELEPRAX: 201-994-1700
TELEPAX: 201-994-1704
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

OTHER INFORMATION: amide-terminated

US-07-908-455A-62
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REGISTATION NUMBER: 24,025
REFERENCE/DOOKET NUMBER: 421250-194
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/226,108
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  US 07686115
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; Sequence 88, Application US/08434120
Patent No. 5635479
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.1%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.1
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||:||:|||
5 KIAKIAKKIAKIAK 18
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLAKLAKKLAKLAK 14
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Sequence 62 Application US/07908455A

Sequence 62 Application US/07908455A

Sequence 62 Application US/07908455A

Sequence 62 Application US/07908455A

GENERAL INFORMATION:

APPLICANT: Berkowitz, Barry A.

APPLICANT: Maloy, W. Lee

TITLE OF INVENTION: USes Therefor

NUMBER OF SEQUENCES: 89

CORRESPONDENCES: APPLESS:

ADDRESSEE: Carchia, Byrne, Bain, Gilfillan,

ADDRESSEE: Cecchi & Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                   STATE: Utah
COUNTRY: USA
ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,455A
FILING DATE: 19920702
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US96/10041 FILING DATE:
                    CORRESPONDENCE ADDRESS:
ADDRESSE: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Sweigert Phb, Susan E
REGISTRATION UNMBER: 36,289
REFERENCE/DOCKET UNMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEFAX: 8015319168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 23 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide;
HYPOTHETICAL: YES
PCT-US96-10041-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLAKLAKKLAKLAK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 KLKKLAKKLAKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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Gaps
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Pred. No. 0.053;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 510 Campus Drive
APPLICANT: 510 Campus Drive
APPLICANT: 910 Lymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner CITRET: 1300 I. Street, N.W. Suite 700 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCEWALTON STATEM.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: US/08/465,325
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFRENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86, Application US/08465325 Patent No. 5686563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                Query Match 87.1%;
Best Local Similarity 71.4%;
Matches 10; Conservative
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE FORRACTERISTICS:
LENGTH: 21 amino acids:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 21 amino acids
                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-434-120-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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MOLECULE TYPE: peptide
US-08-465-325-86
                                                                                                                                                                                                                                                                                                                                                  1 KLAKLAKKLAKLAK 14
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5 KIAKIAKKIAKIAK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                         TYPE: amino acid STRANDEDNESS:
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20005-3315
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87.1%; Score 54; DB 1;

Query Match

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Gaps
              ;
0
71.4%; Pred. No. 0.053;
tive 4; Mismatches 0; Indels
Best Local Similarity 71.4
Matches 10; Conservative
                                                           |:||:||:||:||
5 KIAKIAKKIAKIAK 18
                                            1 KLAKLAKKLAKLAK 14
                                             ò
                                                                        Db
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Search completed: May 8, 2002, 07:19:01 Job time: 69 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

May 8, 2002, 07:17:47 ; Search time 38.66 Seconds (without alignments) 26.824 Million cell updates/sec Run on:

US-09-765-086-200 . 62 1 KLAKLAKKLAKLAK 14

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A_Geneseq_1101:*

/SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseqgpeneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseqgeneseqp/AA1983.DAT:*
/SIDS8/gcgdata/geneseqgeneseqp/AA1983.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1989.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1990.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1991

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Minimalist lytic p	Antimicrobial pro-	Synthetic anti-mic	Lytic peptide with	Minimalist lytic p	Minimalist lytic p	Minimalist lytic p	Homing antimicrobi	Homing antimicrobi	Prostate-homing pr	Homing pro-apoptot
SUMMARIES			a	AAW62925	AAB21900	AAE06478	AAR07747	AAW62942	AAW62922	AAW62926	AAB21936	AAB21939	AAE06512	AAE06514
			DB	19	21	22	11	19	19	19	21	21	22	22
		Query	Length	14	14	14	21	21	21	21	21	21	21	21
	dР	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	62	62	62	62	62	62	62	62	62	62	62
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₽.₩ .⊶	Homing antimicrobi Homing pro-apoptot Minimalist lytic p Minimalist lytic p Minimalist lytic p		> ∪ ∪ →	Ion-channel formin Ion channel formin Peptide used to ma Peptide enhancer o Synthetic anti-neo Lytic peptide used Synthetic lytic pe Lytic peptide with Basic (positively Basic (positively
AAE06515 AAR07741 AAB21938 AAE06513 AAB21940 AAE06517	AAB21937 AAE06516 AAW62943 AAW62923 AAW62927	AAN02941 AAN07743 AAR13821 AAR45107 AAR36366	AAR35357 AAR39069 AAR5963 AAR50539 AAR56924 AAR56924	AAR890129 AAR83902 AAR10725 AAR84167 AAR84167 AAR872416 AAR89973 AAR807737 AAR45051
22 22 22 22 22 23	130 130 130 130 130 130 130 130 130 130	112444	112525	116 120 177 117 141 141
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12 13 14 15 16	19 22 22	25 25 26 27 28 28 28		338 338 344 34 34 34 34 34 34 34 34

ALIGNMENTS

Lytic peptide; channel forming peptide; antibacterial; amphipathic. AAW62925 standard; peptide; 14 AA (first entry) Minimalist lytic peptide. 02-OCT-1998 AAW62925; AAW62925 RESULT

94US-0232525. 96US-0681075. 97US-0789077. 97US-0944133. 97US-0944133 22-APR-1994; 22-JUL-1996; 03-FEB-1997; 06-OCT-1997; 06-OCT-1997; US5789542-A 04 - AUG - 199 Synthetic

(LOUU) UNIV LOUISIANA STATE & AGRIC & MECH COLL. McLaughlin ML; Becker CL,

WPI; 1998-446183/38.

Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-mer lytic peptides

Gaps

.. 0

Length 14; Indels

100.0%; Score 62; DB 21; 100.0%; Pred. No. 0.0029; 0; Mismatches

Conservative 14

14 AA;

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useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such antimicrobial peptide, which can be conjugated to a homing peptide to make the homing pro-apoptotic conjugates of the present invention. The present sequence has an amphipathic alpha-helical structure.
                                                                                                                                                                                                                                                                               1 KLAKLAKKLAKLAK
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                  charged amino acid residues, or five nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
                                          AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                     Length 14;
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                                                                                                                                                                                                                                                                                                                                     100.0%; Score 62; DB 19; 100.0%; Pred. No. 0.0029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial pro-apoptotic peptide #1.
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    Claim 3; Column 35; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21900 standard; Peptide; 14 AA
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Best Local Similarity
                                                                                                                                                                                                                                                                             14 AA;
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Matches
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a synthetic anti-microbial peptide having an amphipathic-alpha helical structure. This peptide is linked to a prostate-homing peptide to generate a chimeric prostate-homing pro-apoptotic peptide.
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                                                                                                                                                                                                         Synthetic anti-microbial peptide #1.
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AAE06478 standard; peptide; 14
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                                                                                                                                                                                                                                                                                                                                        cytostatic.
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Query Match
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Matches 14; Conserv
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22-JUL-1996;
03-FEB-1997;
06-OCT-1997;
                                                                              22-JUL-1996;
03-FEB-1997;
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                US5789542-A.
                                 04 - AUG - 1998
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                         Lysis; neoplastic cells; microbial infections; HIV; P.falciparum; wound healing; adjuvant; hBFSP.
                                                                                                                                                                                                                                                                                                              New lytic polypeptide(s) with proliferative activity - are alpha-helical peptide(s) having aligned amphipathy for treating microbial infections and lysing cancer cells
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                                                                                                                        Lytic peptide with proliferative activiy.
                                                                   AAR07747 standard; protein; 21 AA.
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Best Local Similarity 100.

Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AA;
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AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and three positively two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues and the positively charged amino acid residues and the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
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                                                                                                                                                                                                                                                                                                                                                                                                         Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
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97US-0789077.
97US-0944133.
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                                                                                                                AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and three positively testiques and the positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues and the positively charged amino acid residues and alternative acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the and the positively charged amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha -helix, whereby the multimer is amphipathic.
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW62920-67 represent minimalist lytic (channel forming) peptides. ?
peptides have antibacterial properties in concentrations not lethal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                               Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-mer lytic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - using 14-mer
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                                                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                   Score 62; DB 19; Length 2
Pred. No. 0.0042;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selective lysis of bacteria amongst mammalian cells or 21-mer lytic peptides
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(LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
                                                                                               Disclosure; Column 5; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAW62926 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                  ch 100.0%;
1 Similarity 100.0%;
14; Conservative 0;
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96US-0681075.
97US-0789077.
97US-0944133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McLaughlin ML;
                      McLaughlin ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimalist lytic peptide.
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                                                                                                                                                                                                                                                                                                                                         1 KLAKLAKKLAKLAK
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                                           WPI; 1998-446183/38
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                     21 AA;
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03-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker CL,
                      Becker CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW62926;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                              AAW62926
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toward mammalian cells. The peptides are heptads (or heptad multimers) charged amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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                                                                                                                                                                                                                                                                                              the alpha -helix, whereby the multimer is amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 62; DB 19; Length 21; 100.0%; Pred. No. 0.0042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Preferably D-form residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antimicrobial pro-apoptotic conjugate #1.
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8..21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB21936 standard; Peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Homo sapiens
Chimeric - Unidentified
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                                                                                                                                                                                                                                                                                                                                                                      21 AA;
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Misc-difference
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1 KLAKLAKKLAKLAK 14
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                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                 AAE06512;
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Jomain
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Jomain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer - \frac{1}{2}
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic;
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                                                                      Query Match 100.0%; Score 62; DB 21; Length 21; Best Local Similarity 100.0%; Pred. No. 0.0042; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Preferably D-form residues"
                                                                                                                                                                                                                                                                                                                               Homing antimicrobial pro-apoptotic conjugate #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                        AAB21939 standard; Peptide; 21 AA.
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homing pro-apoptotic conjugate.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                   1 KLAKLAKKLAKLAK 14
                                                                                                                                               Misc-difference 8..21
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                            alpha-helix; human.
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                             21 AA;
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                                                                                                                                                                                                                                                                      AAB21939;
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                             Sequence
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic; HPP-1.
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/label= Membrane_disrupting_domain
/label= Membrane_disrupting; This region forms an
mphipathic helix and is useful in imparting increased
stability of the conjugate in vivo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and a patient with prostate cancer. The present sequence is chimeric prostate-homing pro-apoptotic peptide, HPP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HM;
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100.0%; Pred. No. 0.0042;
iive 0; Mismatches 0;
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/note= "Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                    Prostate-homing pro-apoptotic peptide, HPP-1.
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/label= Homing_domain
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                                                                                                                                                                AAE06512 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                         25-SEP-2001 (first entry)
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Best Local Similarity 100.

Matches 14; Conservative
21
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14; Conservative

100.0%; Score 62; DB 21; Length 21; 100.0%; Pred. No. 0.0042;

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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
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/label= Coupling_domain
/note= "Glycinylglycine bridge"
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/label= Antimicrobial_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Homing_domain
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                                                        AAE06515 standard; peptide; 21 AA
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Best Local Similarity
Matches 14; Conserv
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  RESULT 12
                                AAE06515
                                                                                                                   NAME OF THE PROOF 
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                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses novel chimeric prostate-homing pro-apoptotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Glycinylglycine bridge"
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/label= Antimicrobial_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Socation/Qualifiers
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                                                                                                                                                                                                AAE06514 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                            Homing pro-apoptotic peptide #1.
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                             1 KLAKLAKKLAKLAK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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Matches 14;
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Ellerby HM;

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                                           The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing proapptotic peptide.
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Example 2; Page 80; 176pp; English.
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23 AA;
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                                22-JAN-1999;
27-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic.
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Domain
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                                                                                                                                                                                                                                                   This peptide is an analogue of a known lytic peptide. It comprises an alpha helical conformation of amino acids. It is effective at lysing e.g. gram-positive and -negative bacteria and mammanian neo-plastic cells, cells infected with intracellular pathogenic micro-organisms such as HIV. It stimulates the proliferation of fibro-blasts and lymphocytes and can be used in wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic;
                                       Lysis; neoplastic cells; microbial infections; HIV; P.falciparum; wound healing; adjuvant; hBFSP.
                                                                                                                                                                                                  New lytic polypeptide(s) with proliferative activity - are alpha-helical peptide(s) having aligned amphipathy for treating microbial infections and lysing cancer cells
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                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 11; Length 23; 100.0%; Pred. No. 0.0046;
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Misc-difference 10..23
/note= "preferably D-form residues"
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                       Lytic peptide with proliferative activiy.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB21938 standard; Peptide; 23 AA.
                                                                                                                                                                                                                                    Claim 17; page 41; 57pp; English
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                                                                                                                90WO-US01945
                                                                                                                                 89US-0336181
       (first entry)
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                                                                                                                                                                                                                                                                                                                                                              14; Conservative
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Chimeric - Unidentified.
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       22-FEB-1991
                                                                                                                10-APR-1990;
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                                                                                409012866-A.
                                                                                                 01-NOV-1990.
                                                                synthetic.
                                                                                                                                                                   Jaynes JM;
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                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local S
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The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The antimicrobial pestide has an emphipathic alpha-helical structure. The conjugates are useful for the tractment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such prostate homing pro-apoptotic conjugate.
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                                                                                                                                                                                                                                                                                                                                                         Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
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100.0%; Pred. No. 0.0046;
iive 0; Mismatches 0;
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10..23
/label= Antimicrobial_peptide
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                                                                                                                                                                                                                  Pasqualini R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 29; Page 108; 118pp; English.
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21-JAN-2000; 2000WO-US01602.
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Best Local Similarity 100.
Matches 14; Conservative
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                                                                                                                                                              Ellerby HM;
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21-JAN-2000; 2000US-0489582.
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1 KLAKLAKKLAKLAK 14 δλ q

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Gaps

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Length 23;

Query Match 100.0%; Score 62; DB 22; Length 2 Best Local Similarity 100.0%; Pred. No. 0.0046; Matches 14; Conservative 0; Mismatches 0; Indels

Search completed: May 8, 2002, 07:18:34 Job time: 47 sec

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Sequence 13, Appl
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Sequence 2
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                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               OM protein - protein search, using sw model
                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                              US-09-765-086-207
                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                              1 SMSIARL 7
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                                                                                               Sequence:
                                                                                                                                      Searched:
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APPLICANT: Russlahti, Penata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: METHOD OF 1999-02-26
EARLIER APPLICATION NUMBER: 0990-02-13
NUMBER OF SEQ ID NOS: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  Sequence 15, sequence 10, sequence 4, A sequence 2, A sequence 2, A sequence 2, A sequence 2, A sequence 20, sequence 1, A sequence 1, A sequence 1, A sequence 10, A sequence 5, A sequ
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Sequence 21, Application US/09042107

Patent No. 6232287

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ROSLAHLI, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892

CURRENT APPLICATION NUMBER: US/09/042,107

CURRENT FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 436

SEQ ID NO 21
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US-09-093-585-15
PCT-US95-09172-10
US-08-810-712-24
US-08-810-712-24
US-08-918-41-2
US-08-918-41-2
US-08-942-673-2
US-09-118-317-2
US-09-118-317-2
US-08-468-249A-20
US-08-313-200-1
PCT-US93-03837-1
US-08-946-55
US-08-465-55
US-08-465-55
US-08-465-55
US-09-041-886-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tentIn Ver. 2.0
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Best Local Similarity 100.
Matches 7; Conservative
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206
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        FEATURE:
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Query Match
Best Local Similarity 71.*.
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SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
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                    Beyer, Stefan
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260 SLSIGRL 266
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 439
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US-08-850-880-2
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-21
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                                                                                                                             Query Match 100.0%; Score 30; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94010
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/045,764A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09045764A
Patent No. 6127178
GENERAL INFORMATION:
APPLICANT: Florio, Monica
TITLE OF INVENTION: Apoptotic Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UCSF98-045
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Patent No. 6225064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTATION NUMBER: 36.627
REPERENCE/DOCKET NUMBER: UCSF'
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.7
Best Local Similarity 83.3
Matches 5; Conservative
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CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
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24 SLSIAR 29
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APPLICANT: Brandt, Petra
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Stewen L
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Hofle, Gerhard
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
TITLE OF INVENTION: heteropolyketide compounds
TITLE OF INVENTION NUMBER: US/09/413,814
CURRENT APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1999-10-07
SEARLIER FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
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Gesellschaft fuer Biotechnologische Forschung mbH
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Pred. No. 3.5e+02;
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APPLICANT: Rezanikoff, William S
APPLICANT: Gorysin, Igor Y
APPLICANT: Zhou, Hong
APPLICANT: Zhou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53703
                         Bristol-Myers Squibb, Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08850880 Patent No. 5925545
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ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960;
TELEPHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-413-814-13
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71.48;
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                                                                                       Score 23; DB 2; Length 476;
Pred. No. 3.8e+02;
1; Mismatches 0; Indels
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Pred. No. 3.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reznikoff, William S
APPLICANT: Goryshin, Igor Y
APPLICANT: York, Dona L
APPLICANT: York, Dona L
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PROTECTION PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REPERENCE/DOCKET NUMBER: 960296.94916
TELECOMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/850,880
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08944916
Patent No. 5948622
GENERAL INFORMATION:
APPLICANT: Reznikoff, William S
                                                                                         76.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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               ; MOLECULE TYPE: protein US-08-850-880-2
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GY: linear
TOPOLOGY: linear
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| 427 MAIARL 432
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427 MAIARL 432
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RESULT

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Lymphocytes and Methods of Use Therefor
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                                        GENERAL INFORMATION:
APPLICANT: Goryshin, Igor Y
APPLICANT: Rezalkoff, William S
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 2; Length 476 Pred. No. 3.8e+02; 1; Mismatches 0; Indels
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APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: from T
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CITY: Chicago Sears Tower, 233 South Wacker Drive
CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960296.94142
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COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: US/08/180,371
Sequence 2, Application US/08814877 Patent No. 5965443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08180371
Patent No. 6254861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BETSON, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.78;
83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-814-877-2
                                                                                                                                                                                                                                                                 53703
FPF
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| 427 MAIARL 432
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21 ALSLARL 27
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5430019-2
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                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Besellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Beser, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Cino, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: heteropolyketide compounds
TITLE OF INVENTION: NUMBER: 1999-10-07
EARLIER FILING DATE: 1999-10-07
BARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE PROFICE PATENTIA VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 4; 1
Pred. No. 4.5e+02;
FILING DATE: 12-JAN-1994
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 906866
FILING DATE: 01 July 1992
ATTORNEY/AGENT INFORMATION:
NAME: GTUBER, LEWIS S.
REGISTRATION NUMBER: 30,060
REFERENCE/POCKET NUMBER: 27620/31668
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (312) 474-0448
TELECX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERIFICS:
LENGTH: 554 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 68, Application US/09413814; Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Sorangium cellulosum US-09-413-814-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             linear
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358 SISMARL 364
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LENGTH: 700
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RESULT

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5430019-2
FALCANT: ROGERS, DAVID T.; WOLFMAN, NEIL M.; SEEHRA, JASBIR S.
TITLE OF INVENTION: HOMOGENEOUS K-FGF AND USE OF THE SAME
TITLE OF INVENTION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: 438,278
FILING DATE: 16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Sequence 2, Application 08/102691
Fatent No. 555903
GENERAL INFORMATION:
APPLICANT: VOSHITOMI, Sumie
APPLICANT: KUROKAMA, TSULOMU
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
CITY: Boston
CITY: Poston
CONMENT OF CONTRESSEE
CONTRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 175;
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Pred. No. 2.2e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE:
COMPUTER: DATE:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/102,691
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, Ronald I
REGISTRATION NUMBER: 30626
REGISTRATION NUMBER: 30626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 428:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200921 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 175 amino acids
amino acid
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Best Local Similarity 57.1.
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USA
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52 ALSLARL 58
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                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: 1
STATE:
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5175383-6
; Patent No. 5175383
APLICANT: LEDBR, PHILIP; MULLER, WILLIAM J.
TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/07/312,641
FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-102-691-1

Sequence 1, Application 08/102691
Fatent No. 5559093
GENERAL INFORMATION:
APPLICANT: KUROKAWA, TSULOMU
APPLICANT: IGARASHI, Koichi
TITLE OF INVENTION: PLATELET-INCREASING AGENT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS 6
ADDRESSEE: CUSHMAN
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANTEL
TITLE OF INVENTION:
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 72
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.3%; Score 22; DB 6; Length 205; Best Local Similarity 57.1%; Pred. No. 2.6e+02; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 3; Length 200
Pred. No. 2.5e+02;
3; Mismatches 0; Indels
                                                                                                                         Sequence 72, Application US/09248335 Patent No. 6096504
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Best Local Similarity 57.1%;
Matches 4; Conservative
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| 184 SLTLARL 190
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52 ALSLARL 58
                    ::1:111
23 ALSLARL 29
1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: maize
US-09-248-335-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SMSIARL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO:6:
; LENGTH: 205
                                                                                                       US-09-248-335-72
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                           ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5175383-6
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Gaps
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APPLICANT: Smallwood, Philip M.
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
CORRESPONDENCE : 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 1; Length 206; Pred. No. 2.6e+02; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5090
TELEPAX: 617/678-5099
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08439725A; Patent No. 5693775 GENERAL INFORMATION:
                                                                                                                                                            SOFTWARE: Patentin Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/102,691
                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4283
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-5400
TELERAX: (617)523-6440
TELEX: 200921 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, ROADLD I
REGISTRATION NUMBER: 30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.38;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-102-691-1
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inear
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; INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-439-725A-13
```

; 0 0; Gaps Query Match 73.3%; Score 22; DB 1; Length 206; Best Local Similarity 57.1%; Pred. No. 2.6e+02; Matches 4; Conservative 3; Mismatches 0; Indels

1 SMSIARL 7 ::|:||| 52 ALSLARL 58 δλ

Dp

Search completed: May 8, 2002, 07:19:02 Job time: 70 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 8, 2002, 13:31:42; Search time 23.87 Seconds Run on:

(without alignments)
71.374 Million cell updates/sec

CHIMERA Title: Perfect score:

23 104 1 SMSIARLGGKLAKLAKKLAKLAK Sednence:

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Chimeric prostate-	Homing antimicrobi	Prostate-homing pr	Homing antimicrobi	Homing pro-apoptot		Homing antimicrobi	Homing pro-apoptot	Homing antimicrobi	Homing pro-apoptot
RIES	_										
SUMMARIES	AAB21938	AAE06513	AAB21936	AAE06512	AAB21939	AAE06514	AAE06515	AAB21940	AAE06517	AAB21937	AAE06516
BB	21	22	21	22	21	22	22	21	22	21	22
å Query Match Length DB	23	23	21	21	21	21	21	25	25	26	26
% Query Match	100.0	100.0	75.0	75.0	71.2	71.2	71.2	71.2	71.2	71.2	71.2
Score	104	104	78	78	74	74	74	74	74	74	74
Result No.	н	7	М	4	2	9	7	8	6	10	11

Minimalis	Minimalist 1	Minimalist 1	يډ	Minimalist		Minimalist	Antimicrobi	Synthetic an	7	ப	Amphiphilic		Amphiphilic pepti	Biologically	Ion channel	O	Amphiphilic p	Peptide whic		(KLAGKLA)3 peptide		Peptide used t	Lytic peptide	Lytic peptid		Amphi		Basic	Basic (po	Amphiphili	Amphiphilic	
AAW62926	AAW62943	~	AAW62927	AAW62942		AAW62925	AAB21900	AAE06478	AAR07747	AAR45051	AAR36310	AAR31081	AAR35299	AAR39013	AAR55905	AAR50481	AAR50365	AAR55620	AAR58965	AAR90073	AAR83844	AAY10669	AAR07741	AAR07743	AAR39066	AAR13818	AAR15665	AAR45049	^	m	33	AAR31079
13	19	19	19	19	19	19	21	22	11	14	14	14	14	14	15	15	15	15	15	16	16	20	11	11	14	12	12	14	14	14	14	14
21	28	28	28	21	21	14	14	14	21	21	21	21	21	21	21	21	21	21	21	21	21	21	23	38	42	21	21	21	21	21	21	21
σ.	σ,	6	6	4	63.5	6	σ.	6	6	6	6	σ,	6	6	6	6	6	6	6	6	9.	9.	٥.	8	8	۲.	7	7	7.	7	57.7	57.7
72	72	72	72	67	99	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	61	61	09	09	09	09	09	09	9
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44

ALIGNMENTS

RESULT

AAB21938 standard; Peptide; 23 AA.

AAB21938;

22-MAR-2001

Prostate homing antimicrobial pro-apoptotic conjugate. (first entry)

Cytostatic; homing.pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.

Chimeric - Homo sapiens. Chimeric - Unidentified.

Key Location/Qualifiers Misc-difference 10..23 /note= "Preferably D-form residues"

WO200042973-A2

27 - JUL - 20.00.

21-JAN-2000; 2000WO-US01602.

99US-0235902. 22-JAN-1999;

(BURN-) BURNHAM INST

Ruoslahti EI; Pasqualini R, Ellerby HM, Bredesen DE,

WPI; 2000-499174/44.

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                                                                                                          The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to anglogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                Homing pro-apoptotic conjugate comprising a tumor homing molecule that
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an
                              selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellerby HM;
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                                                                                                                                                                                                                                                                                                                                                           Length 23;
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                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 104; DB 21;
100.0%; Pred. No. 7.1e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Coupling_domain
/note= "Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Prostate_homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10..23
/label- Antimicrobial_peptide
                                                                                                                                                                                                                                                                               prostate homing pro-apoptotic conjugate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                            Claim 29; Page 108; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruoslahti EI, Pasqualini R,
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                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                            23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to anglogenic vasculature. The antimicrobial peptide has low mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
                                          The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo to a prostate cancer, to a patient with prostate cancer. The present sequence is a chimeric prostate-homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic;
                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                               Length 23;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                               Score 104; DB 22;
Pred. No. 7.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homing antimicrobial pro-apoptotic conjugate #1.
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 105; 118pp; English.
             Claim 6; Page 103; 176pp; English.
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                                                                                                                                                                                                                                                                             100.0%; Some 100.0%; Pour 100.0%; Pour 100.0%; Pour 100.0%;
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                                                                                                                                                                                                                                                                                                                                               1 SMSIARLGGKLAKLAKKAK 23
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                                                                                                                                                                                                                                                                                                                 Conservative
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Chimeric - Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-helix; human.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                 23 AA;
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toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial_peptide; prostate cancer; breast tumour homing molecule;
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/label= Membrane_disrupting_domain
/label= Mantimicrobial peptide; This region forms an
amphipathic helix and is useful in imparting increased
stability of the conjugate in vivo"
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                   Score 78; DB 21; Length 21;
Pred. No. 4.2e-05;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                   75.0%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE06512 standard; peptide;
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                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; HPP-1.
                                                                                                                                                        21 AA;
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Local Sim.
17;
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                                                                                                                                                           Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer-
to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is chimeric prostate-homing pro-apoptotic peptide, HPP-1.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposl's sarcoma; amphipathic; alpha-helix; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to homing pro-apoptotic conjugates,
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0
                                                                                                                          Length 21;
                                                                                                                                                       Indels
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/note= "Preferably D-form residues"
                                                                                                                         DB 22;
4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                         Homing antimicrobial pro-apoptotic conjugate #3.
                                                                                                                                                       0; Mismatches
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                                                                                                                          Score 78;
                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 A.
                                                                                                                                                                                                                                                                                                 AAB21939 standard; Peptide; 21
                                                                                                                         75.0%;
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                                                                                                                                                                                      6 RLGGKLAKLAKKLAK 23
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                                                                                                                                         Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                     - Homo sapiens
- Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-499174/44.
                                                                           21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                            22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
Chimeric
                                                                               Sequence
                                                                                                                            Query Match
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                              Homing pro-apoptotic peptide #2.
                                                                               AAE06515 standard; peptide;
                                                                                                                                   (first entry)
 6 ggklaklakklaklak 21
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                                                                                                                                                                                                                                          Unidentified
                                                                                                                                   25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                               cytostatic.
                                                                                                         AAE06515;
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                                                                                                                                                                                                                                                                    Key
Domain
                                                                                                                                                                                                                                                                                                           Domain
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Matches
                                                      RESULT
                                                                   AAE065
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                                                                                                                                                                                                                                                     Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing pro-
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HM;
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DB 21; Length 21; 0.00016;
                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    . Coupling_domain
"Glycinylglycine bridge"
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Glycinyİglycine bridge
8..21
/label= Antimicrobial_peptide
Score 74; DB 2; Pred. No. 0.00 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arap W,
                                                                                                                                                                                                                                                                                                                                                      l...
/label= Homing_domain
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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100.0%; Pre
                                                                                                                                              AAE06514 standard; peptide; 21 AA.
 71.20,
100.08; Pro
0;
                                                                                                                                                                                                                            Homing pro-apoptotic peptide #1.
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                                                                                                                                                                                                  (first entry)
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                          Conservative
                                                    8 GGKLAKLAKKLAK 23
                                                                  6 ggklaklakklaklak 21
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            Best_Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                               cytostatic
                                                                                                                                                                       AAE06514;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and to treat a patient with prostate cancer. The present sequence is a homing proapptotic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses novel chimeric prostate-homing pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ellerby HM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel chimeric prostate-homing pro-apoptotic peptide, used t
prostate cancer, comprises a prostate-homing peptide linked
antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
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100.0%; Pred. No. 0.00016;
ive 0; Mismatches 0;
                                                                                         /label= Coupling_domain
/note= "Glycinylglycine bridge"
                                                                                                                                           8..21
/label= Antimicrobial_peptide
                             1..5
/label= Homing_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arap W,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 80; 176pp; English.
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                                                                                                                                                                                                                                                                                                              16-JAN-2001; 2001WO-US01362.
                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0489582
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nes 16; Conserv
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Length 21;

Score 74; DB 2 Pred. No. 0.00 0; Mismatches

Query Match 71.2 Best Local Similarity 100. Matches 16; Conservative

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Ruoslahti EI,
                                                                                                   Jnidentified
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                                                              cytostatic.
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer -
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                                                                                                                                                                            Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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                                                                                                                                                                                                                                                                                                                                           12..25
/note= "Preferably D-form residues"
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Pred. No. 0.00019;
0; Mismatches 0;
                                                                                                                                       Homing antimicrobial pro-apoptotic conjugate #4.
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                                                                                                                                                                                                                                                                                                         Location/Qualifiers 12..25
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                  AAB21940 standard; Peptide; 25 AA.
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100.0%; Pre
0;
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                           Chimeric - Homo sapiens.
Chimeric - Unidentified.
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                                                                                               22-MAR-2001
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AAB21940
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Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial; breast; prostate; melanoma; cancer; Kaposi's sarcoma; amphipathic; alpha-helix; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arap W, Bredesen DE,
                                                                                                                                                                                                                                                                                           10..11
/label= Coupling_domain
/note= "Glycinylglycine bridge"
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                                                                                                                                                                                                                                                                                                                                                       /note= "Glyčinyľglycine bridge
12..25
/label= Antimicrobial_peptide
                                                                                                                                                                                                                                     ...9
/label= Homing_domain
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 82; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2001; 2001WO-US01362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000; 2000US-0489582
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AA;
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Domain
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                                                                                                                                                                                                                                                                    The present invention relates to homing pro-apoptotic conjugates, comprising of a tumour homing molecule that selectively homes to a mammalian cell type or tissue, linked to an antimicrobial peptide. The homing pro-apoptotic conjugates are selectively internalised by the mammalian cell type or tissue and exhibits high toxicity, especially to angiogenic vasculature. The antimicrobial peptide has low mammalian cell toxicity when not linked to the tumor homing molecule. In addition, the antimicrobial peptide has an amphipathic alpha-helical structure. The conjugates are useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and prostate cancer or melanoma. The present sequence is one such homing pro-apoptotic conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide; antimicrobial peptide; prostate cancer; breast tumour homing molecule; cytostatic.
                                                                                                                                                                                                             Homing pro-apoptotic conjugate comprising a tumor homing molecule that selectively homes to a mammalian cell type or tissue linked to an antimicrobial peptide, useful for the treatment of prostate cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                       Ruoslahti EI;
                          Key Location/Qualifiers
Misc-difference 13..26
/note= "Preferably D-form residues"
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/label= Coupling_domain
/note= "Glycinylglycine bridge"
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                                                                                                                                                                       Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Homing_domain
                                                                                                                                                                                                                                                  Claim 13; Page 105; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE06516 standard; peptide; 26 AA.
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100.0%;
                                                                                                           21-JAN-2000; 2000WO-US01602
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                                                                                                                                                                     Ellerby HM, Bredesen DE,
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- Homo sapiens
- Unidentified
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                                                                                                                                                                                         WPI; 2000-499174/44.
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Best Local Similarity
Matches 16; Conserv
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                                                                   WO200042973-A2
                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                             22-JAN-1999;
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                                                                                       27-JUL-2000
Chimeric
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The patent discloses novel chimeric prostate-homing pro-apoptotic peptide which comprises a prostate-homing peptide linked to an antimicrobial peptide, where the chimeric peptide is selectively internalised by and exhibits high toxicity to prostate tissue and where the antimicrobial peptide has low mammalian cell toxicity when not linked to prostate-homing peptide. The chimeric peptide is used to direct an antimicrobial peptide in vivo to a prostate cancer, to induce selective toxicity in vivo in a prostate cancer, and a patient with prostate cancer. The present sequence is a homing pro-apoptotic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric prostate-homing pro-apoptotic peptide, used to treat prostate cancer, comprises a prostate-homing peptide linked to an antimicrobial peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                                                                                                                                                                                                          Ellerby HM;
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Pred. No. 0.0002;
0; Mismatches 0; Indels
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13..26
/label= Antimicrobial_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 80; 176pp; English.
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96US-0681075.
97US-0789077.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimalist lytic peptide.
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                                                                        WO200153342-A1
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.03-FEB-1997;
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                                                                                                                         26-JUL-2001
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Query Match
Best Local Similarity
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03-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                peptides have antibacterial properties in concentrations for lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively charged amino acid residues. The nonpolar amino acid residues are nonpolar manno acid residues and two positively charged amino acid residues. The nonpolar amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lie on one face of the alpha-helix, and the positively charged amino acid residues will lie on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW62920-67 represent minimalist lytic (channel forming) peptides. The peptides have antibacterial properties in concentrations not lethal toward mammalian cells. The peptides are heptads (or heptad multimers) that comprise four nonpolar amino acid residues and three positively
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                    AAW62920-67 represent minimalist lytic (channel forming) peptides.
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                                                          Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
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                                                                                                                                                                                                                                                                                                                                                             69.2%; Score 72; DB 19; Length 21; 80.0%; Pred. No. 0.00032; ive 2; Mismatches 2; Indels
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                                                                                                       Disclosure; Column 5; 25pp; English.
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96US-0681075.
97US-0789077.
97US-0944133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0944133
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimalist lytic peptide
McLaughlin
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                             WPI; 1998-446183/38
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22-JUL-1996;
03-FEB-1997;
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 Becker CL,
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charged amino acid residues, or five nonpolar amino acid residues and two positively charged amino acid residues. The nonpolar amino acid residues and the positively charged amino acid residues are distributed within the heptad such that when the multimer forms an alpha-helix the nonpolar amino acid residues will lite on one face of the alpha-helix, and the positively charged amino acid residues will lite on the opposite face of the alpha-helix, and the positively charged amino acid residues will lite on the opposite face of the alpha-helix, whereby the multimer is amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
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                                                                                                                                                                                                                                                                                                                                                      Length 28;
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80.08; Pred. No. 0.00042;
Mismatches 2;
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Pred. No. 0.00042;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McLaughlin ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 IARLGGKLAKLAKKLAKLAK
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                               28 AA;
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lytic peptide; channel forming peptide; antibacterial; amphipathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selective lysis of bacteria amongst mammalian cells – using 14-mer or 21-mer lytic peptides
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Pred. No. 0.00042;
2; Mismatches 2; Indels
   2; Indels
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   Mismatches
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                                                                                                                                                                                                                                                                                                   AAW62927 standard; peptide; 28 AA.
5;
                                                               94US-0232525.
96US-0681075.
97US-0789077.
97US-0944133.
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80.0%;
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Best Local Similarity 80.0
Matches 16, Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimalist lytic peptide.
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22-JUL-1996;
03-FEB-1997;
06-OCT-1997;
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         AAW62927;
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Matches
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